

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: <u>05-07-02</u>	Search Site	Vendors
Searcher: <u>Reverly, C. 4414</u>	<u>STC</u>	<u>STN</u>
Terminal time: <u>20</u>	<u>CM-1</u>	<u>Dialog</u>
Elapsed time: _____	<u>Pre-S</u>	<u>APS</u>
CPU time: _____	Type of Search	<u>Geninfo</u>
Total time: <u>2.8</u>	<u>N.A. Sequence</u>	<u>SDC</u>
Number of Searches: _____	<u>A.A. Sequence</u>	<u>DARC/Questel</u>
Number of Databases: <u>1</u>	<u>Structure</u>	<u>Other CGN</u>
	<u>Bibliographic</u>	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 16:24:41 ; Search time 117.39 seconds
(without alignments)
161,536 Million cell updates/sec

Title: US-09-534-229C-1

Perfect score: 1362

Sequence: 1 MARFAALAYCAAAALLAVAA.....MLGTATGGLDVCYQTNFAS 256

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	256	22	AA1987
2	1277	93.8	252	20	AA1988
3	1196	87.8	230	20	AA1989
4	992	72.8	252	21	AA1990
5	846.5	62.2	253	16	AA1991
6	822.5	60.4	253	16	AA1992
7	816.5	59.9	250	16	AA1993
8	814.5	59.8	254	12	AA1994
9	814.5	59.8	254	18	AA1995
10	814.5	59.8	254	21	AA1996
11	798	58.6	323	22	AA1997

12	772	56.7	266	15	AARS2577	Chitinase G. Hord
13	756.5	55.5	292	18	AAW24554	Chitinase. Cucurb
14	747.5	54.9	336	13	AAAR29019	RGH10 chitinase pr
15	747.5	54.9	336	16	AAAR67969	Rice chitinase. O
16	737.5	54.1	259	21	AAAB18902	A maize chitinase
17	737.5	54.1	336	22	AAAB67444	Amino acid sequenc
18	736	54.0	298	20	AAAR98080	Rye chitinase-like
19	736	54.0	318	20	AAAR98079	Rye chitinase-like
20	734	53.9	319	22	AAAB11489	Wheat chitinase pr
21	731	53.7	317	17	AAAW00186	American elm chiti
22	728	53.5	243	20	AAAR90169	C. ensiformis chit
23	710.5	52.2	328	13	AAAR20822	Sequence of endoch
24	710.5	52.2	329	15	AAAR56860	Endochitinase prec
25	707.5	51.9	324	12	AAAR13275	Tobacco intracellu
26	707.5	51.9	324	18	AAAB31297	Nicotiana sp. intr
27	707.5	51.9	324	21	AAAB07513	Amino acid sequenc
28	701	51.5	329	12	AAAR15841	Basic chitinase 48
29	697	51.2	331	12	AAAR11305	Chitinase encoded
30	658	48.3	328	19	AAW64776	Floral organ-speci
31	648.5	47.6	303	13	AAAR20820	Sequence of a 302
32	629	46.2	439	13	AAAR28150	Sugar beet chitina
33	610.5	44.8	272	21	AAAG28415	Arabidopsis thalia
34	610.5	44.8	280	21	AAAG28414	Arabidopsis thalia
35	602	44.2	284	21	AAAB18905	A maize chitinase
36	594.5	43.6	2466	20	AAV05844	Banana ripening fr
37	474	34.8	372	22	AAAB28798	protein encoded by
38	462.5	34.0	155	21	AAAB18906	Amino acid sequenc
39	407.5	29.9	268	13	AAAR28147	Sugar beet chitina
40	398.5	29.3	281	21	AAAB18894	A maize chitinase
41	389.5	28.6	271	21	AAAB18904	Amino acid sequenc
42	389.5	28.6	271	21	AAAB18936	Sugar beet chitina
43	383.5	28.2	264	13	AAAR28145	S. lavendulae MmcY
44	366	26.9	271	21	AAAB32539	Chitinase amino ac
45	337	24.7	294	21	AAAB35811	

ALIGNMENTS

RESULT 1

AA1987
ID AB11487 standard; protein; 256 AA.
XX AA11487;
XX AC
XX 02-MAR-2001 (first entry)
XX Wheat chitinase protein homologous to barley chitinase.
XX Wheat; chitinase; low temperature expression; hardened; plant;
XX snow mould resistance; psychophilic plant pathogen; barley.
XX Triticum aestivum.
XX OS
XX JP2000270866-A.
XX PN
XX 03-OCT-2000.
XX PD
XX 25-MAR-1999; 99JP-0081694.
XX PF
XX 25-MAR-1999; 99JP-0081694.
XX PR
XX (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
XX PA
XX WPI; 2001-027417/04.
XX DR
XX New low temperature expression chitinase gene for producing a plant
XX grade highly resistant to psychophilic plant pathogenic microbes
XX PT
XX Claim 1; Fig 1; lipp; Japanese.
XX PS
XX This invention describes novel wheat chitinase genes. The invention also
XX describes a method for the isolation of a low temperature expression
CC

CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat P1173438 (of high snow mould resistance). The genes are
 CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.

SQ Sequence 256 AA;
 Query Match 100.0%; Score 1362; DB 22; Length 256;
 Best Local Similarity 100.0%; Pred. No. 8.4e-127;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARFALAVCAALLAVAGAAAGVGVSTRSVYASMLPNRNSLCPARGFTYDAF 60
 DB 1 marfaalavcaallavagaaagvgvstrsvyasmplnrnslcpargfitydaf 60
 QY 61 IAAANTFPGFTGSGADDIKRDLAAPFGOTSHETTGTRGAADQFGWGYCFKEEISKATS 120
 DB 61 iaanantfpgftgsgaddikrdlaaifgtshtgtrgaadqfgwgycfkeeiskats 120
 QY 121 PPYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAQGNKPSK 180
 DB 121 ppygrgpiqltgrsnydiag-raigkdlvsnpdlvstdavvsfrfamtawmtaagnkpsk 180
 QY 181 HNVALLRRWPTAADTAAGRPVPGYGVITNIINGLCEGMRNDANVDRIGYTRYCGMLGT 240
 DB 181 hnvalrrwtptaadtaagrpgygvitniinglcegmgrndanvdrigyytrycgmlgt 240
 QY 241 ATGGNLDYTORNFAS 256
 DB 241 atggnldcytgrnfas 256

RESULT 2
 AAW98081
 ID AAW98081 standard; Protein; 252 AA.
 AC AAW98081;
 DT 21-JUN-1999 (first entry)
 XX Rye chitinase-like protein CHW46 preprotein.
 DE CHW46; chitinase-like protein; antifreeze protein; AFP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.
 XX Secale cereale.
 OS Secale cereale.
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /note= "signal peptide"
 FT 23..252
 XX /note= "mature protein, also claimed in Claim 10"
 FN WO9906565-A2.
 XX 11-FEB-1999.
 PD 31-JUL-1998; 98WO-CA00745.
 XX 31-JUL-1997; 97US-0903872.
 XX (ICEB-) ICE BIOTECH INC.
 XX Griffith M, Hew C, Moffatt B, Xiong F;
 XX WPI; 1999-153795/13.
 DR N-PSDB; AAX24890.
 XX New nucleic acid encoding antifreeze polypeptides from plants -
 PT particularly with chitinase activity, used to impart frost, and
 PT pathogen, resistant to plants, for preservation of foods, cells etc.

PT and for treating tumours
 XX Claim 10; Fig 22d; 118pp; English.
 XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
 CC CHW46 preprotein. The mature protein, which is also claimed, is a
 CC chitinase-like protein that has chitinase (antifungal) and
 CC antifreeze activities. CHW46 cDNA (see AAX24890) was obtained by
 CC isolating mRNA from rye plants grown at low temperatures in the
 CC absence of pathogens or other stresses, i.e. under conditions when
 CC only chitinases with antifreeze activity would be expressed.
 CC CHW46 and CHT9 (see AAW98079-80) have been cloned and expressed in
 CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
 CC The chitinase-like antifreeze proteins can be used to increase
 CC freezing tolerance of plants and microorganisms; to increase field
 CC survival of plants, animals and microorganisms exposed to sub-zero
 CC temperatures; to inhibit ice recrystallisation in biological
 CC materials or foods; for cryopreservation and hypothermic protection
 CC of cells, embryos, tissues etc. (particularly human platelets); and
 CC to kill tumour cells. They are also used to inhibit initiation and
 CC progression of diseases or spoilage caused by low temperature
 CC pathogens (particularly fungi) in plants, frozen foods and any
 CC cryopreserved biological material. The signal peptide can be used
 CC to direct protein secretion in transgenic organisms or expression
 CC systems.
 XX Sequence 252 AA;
 SQ

Query Match 93.8%; Score 1277; DB 20; Length 252;
 Best Local Similarity 93.8%; Pred. No. 2.1e-118;
 Matches 240; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARFALAVCAALLAVAGAAAGVGVSTRSVYASMLPNRNSLCPARGFTYDAF 60
 DB 1 marfaal-----aalllavavgaagvgvstrsvyasmplnrnslcpargfitydaf 56
 QY 61 IAAANTFPGFTGSGADDIKRDLAAPFGOTSHETTGTRGAADQFGWGYCFKEEISKATS 120
 DB 57 iaanantfpgftgsgaddikrdlaaifgtshtgtrgaadqfgwgycfkeeinkats 116
 QY 121 PPYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAQGNKPSK 180
 DB 117 ppygrgpiqltgrsnydiag-raigkdlvsnpdlvstdavvsfrfamtawmtaagnkps 176
 QY 181 HNVALLRRWPTAADTAAGRPVPGYGVITNIINGLCEGMRNDANVDRIGYTRYCGMLGT 240
 DB 177 hnvalrrwtptaadtaagrpgygvitniinglcegmgrndanvdrigyytrycgmlgt 236
 QY 241 ATGGNLDYTORNFAS 256
 DB 237 atggnldcytgrnfas 252

RESULT 3
 AAW98082
 ID AAW98082 standard; Protein; 230 AA.
 AC AAW98082;
 DT 21-JUN-1999 (first entry)
 XX Rye chitinase-like protein CHW46.
 DE CHW46; chitinase-like protein; antifreeze protein; AFP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.
 XX Secale cereale.
 OS WO9906565-A2.
 FN 11-FEB-1999.
 PD

KW beta-1,3-glucanase gene.

KW beta-1,3-glucanase gene.


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Db 245 cyngrnfa 252

RESULT 11
AAB11488
ID AAB11488 standard; protein; 323 AA.
AC AAB11488;
XX
XX 02-MAR-2001 (first entry)
XX
XX Wheat chitinase protein homologous to rye chitinase.
XX
XX Wheat; chitinase; low temperature expression; hardened; plant;
XX snow mould resistance; psychophilic plant pathogen; rye.
XX
XX Triticum aestivum.
XX
XX JP2000270866-A.
XX
XX 03-OCT-2000.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
XX
XX WPI; 2001-027417/04.
XX
XX New low temperature expression chitinase gene for producing a plant
XX grade highly resistant to psychophilic plant pathogenic microbes -
XX Claim 4; Fig 2; 11pp; Japanese.
XX
XX This invention describes novel wheat chitinase genes. The invention also
XX describes a method for the isolation of a low temperature expression
XX chitinase gene in which the mRNA is extracted from a fully hardened
XX autumn wheat P17438 (of high snow mould resistance). The genes are
XX useful for creating a plant grade, highly resistant to psychophilic plant
XX pathogenic microbes.
XX
XX Sequence 323 AA;

Query Match 58.8%; Score 798; DB 22; Length 323;
Best Local Similarity 59.8%; Pred. No. 8.3e-71;
Matches 149; Conservative 27; Mismatches 54; Indels 20; Gaps 3;

QY 22 GAAAGGVGVITRSVYASMLPNRDNLSLCPARGFTYDAFIAAANTFPGFTGSADDIKR 81
Db 70 ggggggvasivrdlferfilhrndaaclargfytydafiaaagafpafgtgldtrkr 129
QY 82 DLAAFFGQTSHTTGGTRGAAD-QFOWGYCFKEISKATSP-----YY 124
Db 130 evaaffgtshttgwptapdpfpfsgycfkqg---qgsppsycdqsdapcpagkqyy 186
QY 125 GRPFIQITGSNVDLAGRATGKDLVSNPDVSTDAVVSFRFAMFWMTAGCNKPSCHNVA 184
Db 187 grpplqlthnyngpagraigvdlinnpdivatdptvafktafwnttqsnkpschdvi 246
QY 185 LRRWPTAAATAAGRVPGYGVITNINGLGECGMGRNDANVDRIGYTRYCGMLGTATGG 244
Db 247 tglwtparadsaagrpgygvitnvinvgiegcmgqndkvadrigfkykrycdifggygn 306
QY 245 NLDCYTORNF 254
Db 307 nldcynqlsf 316

RESULT 12
AAR52577
ID AAR52577 standard; Protein; 266 AA.

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XX AAR52577;
XX
XX 05-DEC-1994 (first entry)
XX
XX Chitinase G.
XX
XX Antifungal; pathogen; resistance; transgenic organism; synergy;
XX crop protection; transgenic plant; chitinase; glucanase;
XX protein synthesis inhibitor; disease.
XX
XX Hordeum vulgare L.
XX
XX DE4234131-A.
XX
XX 21-APR-1994.
XX
XX 09-OCT-1992; 92DE-4234131.
XX
XX 09-OCT-1992; 92DE-4234131.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Chet I, Eckes P, Gornhardt B, Jach G, Logemann J;
XX Mundy J, Schell J, Goernhardt B;
XX
XX WPI; 1994-136599/17.
XX
XX N-PSDB; AAQ62518.
XX
XX Transgenic organisms contg. at least 2 pathogen inhibiting genes
XX - esp. plants contg. genes with antifungal activity, show
XX synergistic increase in disease resistance, also new DNA transfer
XX vectors
XX
XX Example 2; Page 13-14; 19pp; German.
XX
XX Chitinase is an enzyme which breaks down chitin, the major protein
XX in insect exoskeletons. The coding sequence may be used in the
XX construction of transgenic organisms, especially plants, to produce
XX pathogen resistant organisms. The genome of such transgenic organisms
XX preferably contains more than one gene with pathogen inhibiting
XX activity, each gene under the control of active promoters. The two
XX gene products then show a synergistic increase in pathogen induced
XX activity so that the transgenic organisms have a greater degree of
XX resistance or resistance against a wider spectrum of diseases.
XX
XX Sequence 266 AA;

Query Match 56.7%; Score 772; DB 15; Length 266;
Best Local Similarity 56.8%; Pred. No. 2.4e-68;
Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps 2;

QY 6 ALAVCAALLLAVAGAAAGGVGVITRSVYASMLPNRDNLSLCPARGFTYDAFIAAAN 65
Db 3 slavvavvatvamaigtargssvsvraqfdmlhrndgacqakgfytydaivaavaa 62
QY 66 TFPFGFTGSADDIKRDLAAFFGQTSHTTGGTRGAAD-QFOWGYCFKEISK----- 117
Db 63 afpfgftgsadackrevaafiaqtshetggwatapdgafawgycfkqergassdyctp 122
QY 118 -----ATSPYVGRGPIQLTGRSNYDLAARATGKDLVSNPDVSTDAVVSFRFAMFWM 171
Db 123 saqwpcpagkryygrgpiqlshnyngpagraigvdlilnnpdivatdatvgfktalwfm 182
QY 172 TAQGNKPSCHNVALRRWPTAAATAAGRVPGYGVITNINGLGECGMGRNDANVDRIGY 231
Db 183 taqpkpschaviagqwspsgadragrvpgfvgvitnlingiegcmgqndkvadrigf 242
QY 232 TRYCGMLGTATGGNLDCYTORNFA 255
Db 243 krycdilgvyggnldcysqrpf 266

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RESULT 13
AAW24554
ID AAW24554 standard; Protein; 292 AA.
XX AC AAW24554;
XX DT 10-OCT-1997 (first entry)
XX DE Chitinase.
XX KW Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase;
KW fungal cell membrane; pathogenic fungi; disease resistance; chitin.
XX OS Cucurbita pepo.
XX PN JP09163987-A.
XX PD 24-JUN-1997.
XX PE 14-DEC-1995; 95JP-0347367.
XX PR 14-DEC-1995; 95JP-0347367.
XX PA (NIHA ) JAPAN ENERGY CORP.
XX PA (SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
XX DR WPI; 1997-380170/35.
XX DR N-PSDB; AAT79940, AAT79941.
XX KW Chitinase derived from pumpkin - used to protect plants against
PT pathogenic fungi
XX PS Claim 1; Page 2; 36pp; Japanese.
XX CC This sequence represents the pumpkin chitinase. Chitinase is an enzyme
CC decomposing chitin (not present in plant cell membranes) found in the
CC cell membranes of fungi. Plants have this enzyme to protect themselves
CC from pathogenic fungi. Thus this enzyme can be used to prevent plants
CC from being infected with pathogenic fungi, and the chitinase gene can be
CC introduced into plants to improve their resistance to diseases caused by
CC fungi. As the amino acid sequence of the chitinase does not have any
CC region to be cleaved by ubiquitous peptidases in cells, the chitinase
CC produced by genetic recombination technology works for various host cells
CC and serves for plant immunity to confer disease resistance on plants as
CC the host.
XX Sequence 292 AA;

Query Match 55.5%; Score 756.5; DB 18; Length 292;
Best Local Similarity 58.3%; Pred. No. 9.4e-67;
Matches 144; Conservative 26; Mismatches 64; Indels 13; Gaps 2;

QY 21 GGAAGQGVSVITRSVYASMLPNRNSLCPARGFTYDAFIAAATFPFGFTGTSADDIK 80
Db 46 ggggggsvsinealynqmlkysxdrpcpsngfyrynafitaagdsfsgftgdaatrk 105
QY 81 RDLAFAFGQTSHETGTRGAAD-QFQWGYCFKEISK-----ATSPPYGRG 127
Db 106 relaaffqgtshettggtatpdygawgycfirennqdvyspqqgwpcasgqkygrg 165
QY 128 PIQLTGRSNYDLAIGKDLVSNPDVSTDAVVSFRFAMFWMTAQGNKPSCHNVALRR 187
Db 166 pqlthnyygpagraalnllonpdlvatpvaftaiwfmtpggnkpschdvtgr 225
QY 188 WPTAADTAAGRVPGVGTNIINGLEGCMGRNANVDRIGYTRYCGMLTATYCGNLD 247
Db 226 wqpsaadsaagrvpgvgtiniinglegcrgdarsvadrifgkrycallygvgnld 285
QY 248 CQTQRNF 254
Db 286 cnnqrnf 292

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RESULT 14
AAR29019
ID AAR29019 standard; Protein; 336 AA.
XX AC AAR29019;
XX DT 20-APR-1993 (first entry)
XX DE RCH10 chitinase protein.
XX KW Promoter; region; rice; chitinase; physical; biological; stress;
KW leaves; stems; roots; male; female; reporter; monocotyledon;
KW dicotyledon; development; plant; defence; selectable; genes.
XX OS Oryza sativa.
XX FH Key
XX FT Region
XX FT 123..323
XX FT Location/Qualifiers
XX FT /note= "Region conserved between class I and class
XX FT II chitinases"
XX PN W09220807-A.
XX PD 26-NOV-1992.
XX PF 21-MAY-1992; 92WO-US04282.
XX PR 22-MAY-1991; 91US-0704288.
XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX PI Lamb CJ, Zhu Q;
XX DR WPI; 1992-415785/50.
XX DR N-PSDB; AAO31407.
XX CC DNA fragment contg. chitinase gene and its regulatory region - is
XX responsive to mature plant stress and has low level expression in
XX leaves, moderate level expression in stem and high level
XX expression in roots
XX PS Disclosure; Page 33-34; 45pp; English.
XX CC The sequence given is encoded by the rice chitinase gene. The promoter
XX region of this gene (see AAO31407) is responsive to physical and/or
XX biological stress. The pattern of expression of this protein in mature
XX plants is characteristic. There is a low level of expression in
XX leaves, a moderate level in plant stems and the highest level in roots
XX and the male and female parts of the plant. The chitinase promoter
XX sequence may be linked to a reporter gene for expression in mono- or
XX dicotyledon plants. Expression of this reporter gene may be used to
XX study patterns of development and controlled expression of plant
XX defence genes and selectable genes.
XX Sequence 336 AA;

Query Match 54.9%; Score 747.5; DB 13; Length 336;
Best Local Similarity 57.3%; Pred. No. 8.8e-66;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGGAAAGQGVSVITRSVYASMLPNRNSLCPARGFTYDAFIAAATFPFGFTGTSADDI 79
Db 70 asggggsgsvaslvrsifdlmllhrndaacpsnfytadafvaasafpgfaaaadadtn 129
QY 80 KRDLAFAFGQTSHETGTRGAAD-QFQWGYCFKEISK-----ATSPPY 124
Db 130 krevaafiaqtshettggwatpdygtwgycfkeengagpdycqgsaqwpcagkky 189
QY 125 GRGPIQLTGRSNYDLAIGKDLVSNPDVSTDAVVSFRFAMFWMTAQGNKPSCHNVA 184
Db 125 GRGPIQLTGRSNYDLAIGKDLVSNPDVSTDAVVSFRFAMFWMTAQGNKPSCHNVA 184

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Db 190 grgpiqlsynfnygpaggaigadllgdpdlvasdatvsfdtafwmtppqspkpscnava 249
QY 185 LRRWPTADTAAGRVPGYGVITNIINGLECCMGGRNDANVDRIGYTRYCGMLGTATGG 244
Db 250 tgqwtpsaddqragrvpgygvitniingglecghgeddrigfykrycdilgvsyga 309
QY 245 NLDCTQR 252
Db 310 nldcysqr 317

RESULT 15
AAR67969
ID AAR67969 standard; Protein; 336 AA.
XX AAR67969;
XX DT 13-AUG-1995 (first entry)
XX DE Rice chitinase.
XX KW Chitinase; transgenic plant; disease resistance;
KW crop improvement; tobacco; Nicotiana tabacum; plant defense;
KW fungus pathogen; Cercospora nicotinae;
KW Thanatephorus cucumeris.
XX OS Oryza sativa.
XX FN WO9502319-A.
XX PD 26-JAN-1995.
XX PF 15-JUL-1994; 94WO-US07815.
XX PR 16-JUL-1993; 93US-0093372.
XX PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX PI Dixon RA, Lamb CJ, Maher EA, Zhu Q;
XX WPI: 1995-067090/09.
XX N-PSDB; AAQ81346.
XX PT Transgenic plants contg. several plant defence associated
PT proteins - have increased resistance to plant pathogens when
PT grown in crops as a food source
XX PS Disclosure; Page 31-32; 45pp; English.
XX CC The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) and
CC an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were
CC incorporated into vectors for co-expression in transgenic tobacco,
CC resulting in improved resistance to Cercospora nicotinae and
CC Thanatephorus cucumeris fungal infection.
XX CC
SQ Sequence 336 AA;

Query Match 54.9%; Score 747.5; DB 16; Length 336;
Best Local Similarity 57.3%; Pred. No. 8.8e-66;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGGAAAGQGVSVITRSVASMILPNRDNLSICPARGFYTDYDAFIAAANTFPGTGSADDI 79
Db 70 asggggsgvasivsrllfdlmlhndaacpasnftydafvaasafpgfaagdadtn 129
QY 80 KRDLAAFFGQTSHETGGTRGAAD-QFQWGYCFKEISK-----ATSPYY 124
Db 130 krevaafiaqtshettggwatpdpdytwgycfkeengagdpdycqqsagwpcaagkyy 189
QY 125 GRGPIQLTGRSYDLAGRAIGDLYSNPLVSTDAVVSPTAMWPMTAGGNKPSCHNVA 184
Db 190 grgpiqlsynfnygpaggaigadllgdpdlvasdatvsfdtafwmtppqspkpscnava 249

QY 185 LRRWPTADTAAGRVPGYGVITNIINGLECCMGGRNDANVDRIGYTRYCGMLGTATGG 244
Db 250 tgqwtpsaddqragrvpgygvitniingglecghgeddrigfykrycdilgvsyga 309
QY 245 NLDCTQR 252
Db 310 nldcysqr 317

Search completed: May 3, 2002, 18:30:29
Job time: 7548 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 18:30:37 ; Search time 79.44 Seconds
(without alignments)
72.518 Million cell updates/sec

Title: US-09-534-229C-1
Perfect score: 1362
Sequence: 1 MARFAALAVCAAAALLAVAA.....MLGTATGGNLDCTQRFNPFAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846.5	62.2	253	1	US-08-162-475A-5
2	838.5	60.8	253	1	US-08-162-475A-2
3	816.5	59.9	250	1	US-08-162-475A-4
4	814.5	59.8	254	1	US-08-047-413-9
5	814.5	59.8	254	3	US-08-229-050-9
6	814.5	59.8	254	3	US-08-801-563-9
7	808.5	59.4	253	4	US-07-791-931-9
8	772	56.7	266	1	US-08-812-025-10
9	772	56.7	266	4	US-07-791-931-10
10	772	56.7	266	4	US-09-138-873A-10
11	747.5	54.9	336	1	US-07-704-288C-3
12	747.5	54.9	336	1	US-08-093-372-2
13	747.5	54.9	336	1	US-08-379-259-3
14	719	52.8	318	1	US-07-704-288C-9
15	719	52.8	318	1	US-08-379-259-9
16	718.5	52.8	328	4	US-07-791-931-7
17	710.5	52.2	329	2	US-08-475-427-13
18	710.5	52.2	329	2	US-07-842-165-13
19	709	52.1	328	4	US-07-791-931-5
20	707.5	51.9	324	4	US-08-047-413-11
21	707.5	51.9	324	3	US-08-229-050-11
22	707.5	51.9	324	3	US-08-801-563-11
23	705.5	51.8	254	2	US-08-475-427-1
24	705.5	51.8	254	2	US-07-842-165-1
25	705.5	51.8	254	4	US-08-448-398-3
26	705.5	51.8	310	4	US-07-791-931-6
27	703	51.6	330	1	US-07-704-288C-8

28	703	51.6	330	1	US-08-379-259-8	Sequence 8, Appli
29	696	51.1	310	1	US-07-704-288C-6	Sequence 6, Appli
30	696	51.1	310	1	US-08-379-259-6	Sequence 6, Appli
31	689.5	50.6	314	1	US-07-704-288C-7	Sequence 7, Appli
32	689.5	50.6	314	1	US-08-379-259-7	Sequence 7, Appli
33	654.5	48.1	302	2	US-08-475-427-6	Sequence 6, Appli
34	654.5	48.1	302	2	US-07-842-165-6	Sequence 6, Appli
35	566.5	41.6	316	4	US-07-791-931-8	Sequence 8, Appli
36	474	34.8	372	4	US-07-791-931-4	Sequence 4, Appli
37	438	31.4	130	3	US-08-329-799-37	Sequence 37, Appli
38	213	15.6	148	3	US-08-329-799-35	Sequence 35, Appli
39	82	6.0	3739	3	US-09-320-878-2	Sequence 2, Appli
40	82	6.0	3739	4	US-09-105-537-33	Sequence 33, Appli
41	82	6.0	11877	4	US-09-105-537-6	Sequence 6, Appli
42	81.5	6.0	249	4	US-09-413-814-100	Sequence 100, App
43	80.5	5.9	285	3	US-09-141-821-1	Sequence 1, Appli
44	79	5.8	922	4	US-08-450-269C-6	Sequence 6, Appli
45	78	5.7	1026	2	US-08-542-003-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-162-475A-5
; Sequence 5, Application US/08162475A
; Patent No. 5656474
; GENERAL INFORMATION:
; APPLICANT: Zohreh Tabaeizadeh
; TITLE OF INVENTION: A novel endochitinase gene
; TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
; TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162.475A
; FILING DATE: December 7, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, Paul E. Jr.
; REGISTRATION NUMBER: 32011
; REFERENCE/DOCKET NUMBER: PEW/3122/204351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Nicotiana tabacum
US-08-162-475A-5

Query Match 62.2%; Score 846.5; DB 1; Length 253;
Best Local Similarity 63.9%; Pred. No. 4.5e-82;
Matches 159; Conservative 32; Mismatches 51; Indels 7; Gaps 3;
QY 6 ALAVCAAAALLAVAGGAAAGVGSVITRSVYASMLPNRDNLCPCARGFTYDAFTAAAN 65
Db 9 ALFCCVFFLELT----GSLAQGIGSVITSDLFNEMLKNRDGRCPANGFTYDAFTAAAN 64

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Qy 66 TFGGTGSGSADDIKRDIAAFGGTSHETTTGGTRGAADQFQWGYCFKKEISKATSPPYIG 125
Db 65 SFPQGTGGDDTARKKEIAAFGGTSHETTTGSL-SAEFFTGGYCFVRQNDQ--SDRIYG 121
Qy 126 KPTOLTGRSNVDLAGRAIGKDIKDVSNPDVSTDAVVSFRTAMFWMTAOGNKPCHNVAL 185
Db 122 KPTOLTNNYKAEATAIGQELVNNPDVATDATISFKTAIWFMTPDQDNKPSHDVII 181
Qy 186 RWTPTAADTAAGRVPGYGVITNIIINGGLECGMRNDANVDRIGYTRYCGMLGTATG 245
Db 182 GRWTPSAADOANRPVPGYGVITNIIINGGIEGIGRNDAVEDRIGYTRYCGMLNVPGEN 241
Qy 246 LDCYQORNF 254
Db 242 LDCYQORNF 250

RESULT 2
US-08-162-475A-2
; Sequence 2, Application US/08162475A
; Patent No. 5656474
; GENERAL INFORMATION:
; APPLICANT: Zohreh Tabaeizadeh
; TITLE OF INVENTION: A novel endochitinase gene
; TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
; TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,475A
; FILING DATE: December 7, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, Paul E. Jr.
; REGISTRATION NUMBER: 32011
; REFERENCE/DOCKET NUMBER: PEW/3122/204351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Lycopersicon chilense
US-08-162-475A-2

Query Match 60.8%; Score 828.5; DB 1; Length 253;
Best Local Similarity 61.6%; Pred. No. 3.7e-60;
Matches 157; Conservative 32; Mismatches 59; Indels 7; Gaps 3;

Qy 3 REAALVCAALLAAGAAGGAGGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIA 62
Db 2 KNTLVSPVALSCLFFLELTGLAQNAGSIVTRELFEOMLSFRNDACPAKGFYTYDAFIA 61
Qy 63 AANTFPFGTGSADDIKRDIAAFGGTSHETTTGGTRGAADQFQWGYCFKKEISKATSP 122
Db 62 AANSEFPFGTGGTTRARKKEIAAFGGTSHETTKGSAGT---FTGGYCFVRQIDQ--SDR 116
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Qy 123 YYGRGPIQLHGRSNVDLAGRAI--GKDLVSNPDVSTDAVVSFRTAMFWMTAOGNKPSC 180
Db 117 YYGRGPIQLHGRSNVDLAGRAI--GKDLVSNPDVSTDAVVSFRTAMFWMTAOGNKPSC 176
Qy 181 HNVALRRTPTAADTAAGRVPGYGVITNIIINGGLECGMRNDANVDRIGYTRYCGMLGT 240
Db 177 HNVIQWTPSPADTAANRPVPGYGVITNIIINGGLECGMRNDANVDRIGYTRYCGMLNV 236
Qy 241 ATGNLDCYQORNF 255
Db 237 PTGENLDCNNKNFA 251

RESULT 3
US-08-162-475A-4
; Sequence 4, Application US/08162475A
; Patent No. 5656474
; GENERAL INFORMATION:
; APPLICANT: Zohreh Tabaeizadeh
; TITLE OF INVENTION: A novel endochitinase gene
; TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
; TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,475A
; FILING DATE: December 7, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, Paul E. Jr.
; REGISTRATION NUMBER: 32011
; REFERENCE/DOCKET NUMBER: PEW/3122/204351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Lycopersicon chilense
US-08-162-475A-4

Query Match 59.9%; Score 816.5; DB 1; Length 250;
Best Local Similarity 62.3%; Pred. No. 6.8e-79;
Matches 154; Conservative 30; Mismatches 56; Indels 7; Gaps 3;

Qy 11 AAILLAVAAGGAAAGGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAANTPPGF 70
Db 7 ALSCLFFLELTGLAQNAGSIVTRELFEOMLSFRNDACPAKGFYTYDAFIAAANSPPGF 66
Qy 71 GTTGSADDIKRDIAAFGGTSHETTTGGTRGAADQFQWGYCFKKEISKATSPPYVGRPIQ 130
Db 67 GTTGDDTARKKEIAAFGGTSHETTINGSGAGT---FTGGYCFVRQIDQ--SDRIYGRPIQ 121
Qy 131 LTGGSNVDLAGRAI--GKDLVSNPDVSTDAVVSFRTAMFWMTAOGNKPCHNVALRRW 188
Db 122 LTHOSNTERAGGQIGVQDVLNPDVATDIIISFKTAIWFMTAHHNKPCHNVIIGQW 181
Qy 189 TPTAADTAAGRVPGYGVITNIIINGGLECGMRNDANVDRIGYTRYCGMLGTATGGNIDC 248
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DB 182 TSPDANRVPYGVITNIINGLEONMGENTAVESRIGYRRYCGMLNVPETGENLDC 241
QY 249 YTORNEFA 255
DB 242 NNCKNEFA 248

RESULT 4
US-08-047-413-9
; Sequence 9, Application US/08047413
; Patent No. 5670706
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/047,413
; FILING DATE: 19-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-047-413-9

Query Match 59.8%; Score 814.5; DB 1; Length 254;
Best Local Similarity 62.1%; Pred. No. 1.1e-78;
Matches 154; Conservative 31; Mismatches 62; Indels 1; Gaps 1;

QY 8 AVCAALLLAVAGGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAATF 67
DB 6 SVLALSFVFLPTGLTQNVGSIVTSLFDQMLKNRDNARCFVAVRFYTYDAFIAANSF 65
QY 68 PFGFTGSADDIKRDLAAFEQGTSHETTGTCGAQDFQWGYCFKEISKATSPPPYVGRG 127
DB 66 PFGFTGDDTARKKEIAFAFFGOTSHETTGTLSPDGPYAGGYCFLE-GNQMGNGIYGRG 124
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QY 128 PIQLTGRSNYDLAIGKDLVSNPOLVSTDAVVSFRTAMFWMTAGNKPSCNVALRR 187
DB 125 PIQLTGOSNYDLAIGKDLVNNPDLVATDATVSEKTAIFWMTFQGNKPSCHDVTGR 184
QY 188 WPTDADTAAGRVPYGVITNIINGLECGMGNDANDVDRIGYTYCYGMLGTATGGLD 247
DB 185 WTPSAADTSANRVPYGVITNIINGIECGKGONARVEDRIGYTYRRNVSMNVAPGDNLD 244
QY 248 CYTORNEFA 255
DB 245 CYNORNEFA 252

RESULT 5
US-08-229-050-9
; Sequence 9, Application US/08229050
; Patent No. 6066491
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-229-050-9

Query Match 59.8%; Score 814.5; DB 3; Length 254;
Best Local Similarity 62.1%; Pred. No. 1.1e-78;
Matches 154; Conservative 31; Mismatches 62; Indels 1; Gaps 1;
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QY 8 AVCAALLLAVAGGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAATF 67


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; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO'10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; US-07-791-931-10

Query Match          56.7%; Score 772; DB 4; Length 266;
Best Local Similarity 56.8%; Pred. No. 4e-74;
Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps

QY 6 ALAVCAALLLVAAGAAAGVGSVITRSVYASMLPNRDNLSLCPARGYTYTDAFTAAAN 65
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Db 3 SLAVVAVAVATVMAIGTARGSVSSVSRQAQFDRMLLHRNDGACQAKGYTYTDAFYAAAA 62
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 66 TFGFGTTGSADDIKRLAAFFGQTSHTETGGTRGAAD-QFOWGYCFKKEISK----- 117
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 63 AFDGFTIGSADQAKREVAFLAQTSHTETGGWATPDGAFANGYCFKQERGASSDYCTP 122
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 118 -----ATSPYYXGRGPIQUTGRNSYDLAGRAIGKDLVSNPOLVSTDAVVVSFTAMFWM 171
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 123 SAQWPCAPGKRYXGRGPIQLSHNYNYGPAGRAIGVDLLANPDILVAITDATVGFKTAIFWM 182
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 172 TAQGNKPSCHNVALRWKTPAATTAAGRVPGYVITNIIINGGLECGMRDANVDRIGY 231
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 183 TAQPKPSHAVTAGQWPSGADRAAGRVGFGVITNIIINGGLECGMRDANVDRIGY 242
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 232 TRYCGMLGTATGGNLDCTQRNEA 255
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 243 KRYCDILGVGYNLDCTYSQRPPA 266
   ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 10
US-09-138-873A-10
; Sequence 10, Application US/09138873A
; Patent No. 6271438
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/138,873A
; APPLICATION NUMBER: US/09/138,873A
; FILING DATE: August 24, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Tenser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 amino acids

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84 AAFPGQTSHTTGTGTRGAAD-QFOWGYCFKKEEISKAT-----SPPYKGRGPIQL 131
123 AAFGLQTSHTTGTGWTAPDGPYAWGYCFYRERNPSTCSATPQPCAPGQOYYGRGPIQI 182
132 TGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAQGNKPSCHNVALRRWPT 191
183 SWNTNYGQCGRGAIQVGLLNKPDVLTDSVTSFKSALWFWMTAQSPKPSHHDVITSRWTPS 242
192 AADTAAGRVPQGYVITNIIINGLCEGMRNDANVDRIYTRYCGMLGTATGNNLDCYTQ 251
243 SADVAARELPQGYVTNIIINGLCEGMRNDANVDRIYTRYCGMLGTATGNNLDCYSQ 302
252 RNFA 256
303 TFFGN 307

Search completed: May 3, 2002, 18:43:02
Job time: 745 sec

84 AAFPGQTSHTTGTGTRGAAD-QFOWGYCFKKEEISKAT-----SPPYKGRGPIQL 131
123 AAFGLQTSHTTGTGWTAPDGPYAWGYCFYRERNPSTCSATPQPCAPGQOYYGRGPIQI 182
132 TGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAQGNKPSCHNVALRRWPT 191
183 SWNTNYGQCGRGAIQVGLLNKPDVLTDSVTSFKSALWFWMTAQSPKPSHHDVITSRWTPS 242
192 AADTAAGRVPQGYVITNIIINGLCEGMRNDANVDRIYTRYCGMLGTATGNNLDCYTQ 251
243 SADVAARELPQGYVTNIIINGLCEGMRNDANVDRIYTRYCGMLGTATGNNLDCYSQ 302
252 RNFA 256
303 TFFGN 307

RESULT 15
US-08-379-259-9
; Sequence 9, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-9

Query Match 52.8%; Score 719; DB 1; Length 318;
Best Local Similarity 53.9%; Pred. No. 2.2e-68;
Matches 132; Conservative 37; Mismatches 64; Indels 12; Gaps 2;
24 AAQGVGVITRSVYASMLPNEDNSLCFARGFYTYDAFTAAANTFPFGTGSADDIKRDL 83
63 APTDLSALISKRSTPDQMLKHNKDGCAPKAGFYTYDAFTAAAKAYPSFGNIGDTRRKREI 122

C;Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S48848
R;Bryngelsson, T.; Collinge, D.B.; Green, B.; Gummeson, P.O.; Kragh, K.; Thordal-Christ
submitted to the EMBL Data Library, March 1994
A;Description: Purification, characterization and cDNA sequence of a basic chitinase fro
A;Reference number: S48847
A;Accession: S48848
A;Molecule type: mRNA
A;Residues: 1-252 <BRI>
A;Cross-references: EMBL:X78672; NID:g563488; PIDN:CAA55345.1; PID:g563489
C;Genetics:
A;Gene: cht2b
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-252/Product: chitinase cht2b #status predicted <Mat>
F:27-251/Domain: plant chitinase homology <PCH>

Db 65 SFPGFGTTGDDTARRKETAIAFFGQTSHETTTGSSL-SAEFFTGGYCFVRQNDQ--SDRYYG 121
QY 126 RGPQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPSCHNVAL 185
Db 122 RGPQLTNRNNYERAGTAIGELVNNPDLVATDATISFKTAIWFWMTAQGNKPSCHNVAL 181
QY 186 RWTPTAADAAGRVPGYGVITNIINGLEGCMGRNDANVDRIYGYRYRYCGMLGTATGNN 245
Db 182 GRWTPSAADQAANRPVPGYGVITNIINGLEGCMGRNDANVDRIYGYRYRYCGMLGTATGNN 241
QY 246 LDCYTQNRNF 254
Db 242 LDCYNQNRNF 250

RESULT 4
S20738
chitinase (EC 3.2.1.14) PR-Q - common tobacco
N;Alternate names: acidic chitinase PR-Q
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S20738
R;Linhorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meu
submitted to the EMBL Data Library, January 1990
A;Description: Constitutive expression of acidic and basic Chitinase in transgenic to
A;Reference number: S20737
A;Accession: S20738
A;Molecule type: mRNA
A;Residues: 1-253 <LIN>
A;Cross-references: EMBL:X51425; NID:g19772; PIDN:CAA35789.1; PID:g19773
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 62.4%; Score 850.5; DB 2; Length 253;
Best Local Similarity 63.9%; Pred. No. 1.7e-66;
Matches 159; Conservative 33; Mismatches 50; Indels 7; Gaps 3;
QY 6 ALAVCAALLAVAAAGAAAGGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFAAAN 65
Db 9 ALFCCVFFLELT---GSLAQIGSVITSDLFNEMLNKNDGRCPPANGFFTYDAFAAAN 64
QY 66 TFPFGTGSADDIKRLAALFFGQTSHETTTGTRGAADQFQWGYCFKEEISKATSPPYG 125
Db 65 SFPGFGTTGDDTARRKETAIAFFGQTSHETTTGSSL-SAEFFTGGYCFVRQNDQ--SDRYYG 121
QY 126 RGPQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPSCHNVAL 185
Db 122 RGPQLTNRNNYERAGTAIGELVNNPDLVATDATISFKTAIWFWMTAQGNKPSCHNVAL 181
QY 136 RWTPTAADAAGRVPGYGVITNIINGLEGCMGRNDANVDRIYGYRYRYCGMLGTATGNN 245
Db 182 GRWTPSAADQAANRPVPGYGVITNIINGLEGCMGRNDANVDRIYGYRYRYCGMLGTATGNN 241
QY 246 LDCYTQNRNF 254
Db 242 LDCYNQNRNF 250

RESULT 5
S37342
chitinase (EC 3.2.1.14) chl17 precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S37342; S38837; S25635
R;Danhash, N.; Wagcmakers, C.A.M.; van Kan, J.A.L.; de Wit, P.J.G.M.
Plant Mol. Biol. 22, 1017-1029, 1993
A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu
A;Reference number: S37341; MUID:94003061
A;Accession: S37342
A;Molecule type: mRNA
A;Residues: 1-247 <DAN>

C;Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S48848
R;Bryngelsson, T.; Collinge, D.B.; Green, B.; Gummeson, P.O.; Kragh, K.; Thordal-Christ
submitted to the EMBL Data Library, March 1994
A;Description: Purification, characterization and cDNA sequence of a basic chitinase fro
A;Reference number: S48847
A;Accession: S48848
A;Molecule type: mRNA
A;Residues: 1-252 <BRI>
A;Cross-references: EMBL:X78672; NID:g563488; PIDN:CAA55345.1; PID:g563489
C;Genetics:
A;Gene: cht2b
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-252/Product: chitinase cht2b #status predicted <Mat>
F:27-251/Domain: plant chitinase homology <PCH>

QY 1 MARFAALVCAALLAVAAAGAAAGGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
Db 1 MARYAAL----RALLAVAVGAAAGGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 56
QY 61 IAAANTFPFGTGSADDIKRLAALFFGQTSHETTTGTRGAADQFQWGYCFKEEISKATS 120
Db 57 IAAANTFPFGTGSADDIKRLAALFFGQTSHETTTGTRGAADQFQWGYCFKEEISKATS 116
QY 121 PPIYGRGPTQLGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPS 180
Db 117 PPIYGRGPTQLGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPS 176
QY 181 HNVALRWPTAADAAGRVPGYGVITNIINGLEGCMGRNDANVDRIYGYRYCGMLGT 240
Db 177 HDVALRWPTAADAAGRVPGYGVITNIINGLEGCMGRNDANVDRIYGYRYCGMLGT 236
QY 241 ATGNLDCYTQNRNFAS 256
Db 237 ATGNLDCYTQNRNFAS 252

RESULT 3
B34801
pathogenesis-related protein Q precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C;Accession: B34801
R;Payne, G.; Ahl, P.; Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A;Title: Isolation of complementary DNA clones encoding pathogenesis-related proteins P
A;Reference number: A34801; MUID:90115914
A;Accession: B34801
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <PAY>
A;Cross-references: GB:M29868; NID:g170313; PIDN:AAA34107.1; PID:g170314
C;Superfamily: plant chitinase; plant chitinase homology
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 62.7%; Score 854.5; DB 2; Length 253;
Best Local Similarity 64.3%; Pred. No. 7.7e-67;
Matches 160; Conservative 32; Mismatches 50; Indels 7; Gaps 3;
QY 6 ALAVCAALLAVAAAGAAAGGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFAAAN 65
Db 9 ALFCCVFFLELT---GSLAQIGSVITSDLFNEMLNKNDGRCPPANGFFTYDAFAAAN 64
QY 66 TFPFGTGSADDIKRLAALFFGQTSHETTTGTRGAADQFQWGYCFKEEISKATSPPYG 125
Db 65 SFPGFGTTGDDTARRKETAIAFFGQTSHETTTGSSL-SAEFFTGGYCFVRQNDQ--SDRYYG 121

A:Cross-references: EMBL:Z15139; NID:g19186; PIDN:CAA78844.1; PID:g19187
A:Accession: S38837
A:Molecule type: protein
A:Residues: 112-115;183-188;218-221 <DA2>
C:Genetics:
A:Gene: ch17
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-247/Product: chitinase ch17 #status predicted <MAT>
F:22-245/Domain: plant chitinase homology <PCH>

Query Match 62.4%; Score 850; DB 2; Length 247;
Best Local Similarity 63.5%; Pred. No. 1.8e-66;
Matches 158; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY 7 LAVCAAAALLVAAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANT 66
Db 1 MVLCCVFLFLT--GSFAQDVGTIVTSDLFNEMLKRNDRCPARGFYTYDAFIAAANS 57

QY 67 PFGFGTGSADDIKRLAFAFGTSHETGTGTRGAADQFQWGYCFKEEISKATSPPYGR 126
Db 58 PFGFGTGGDDTARKKETAFAFGTSHETGTGSLASDGPFAGGCFVREGNQMS-GEYGR 116

QY 127 GPIQLTGRSNYDLAAGRAIGKDIYNSPDLVSTDAVVSFRTAMFWMTAOGNKPCHNVALR 186
Db 117 GPIQLTGSQNYDLAAGRAIGKDIYNSPDLVSTDAVVSFRTAMFWMTAOGNKPCHNVALR 176

QY 187 RWTPTAADTAAGRPVGVITNIINGLEGCMGRNDANVDRIYTRYCYGMLGTATGNL 246
Db 177 QWTPSAADASANRQPGYGVITNIINGLEGCMGRNDANVDRIYTRYCYGMLGTATGNL 236

QY 247 DCYTORNFA 255
Db 237 DCYDQORNEA 245

RESULT 6
S51589
Chitinase (EC 3.2.1.14) pcht28 precursor - Lycopersicon chilense
N:Alternate names: endochitinase pcht28
C:Species: Lycopersicon chilense
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S51589
R:Chen, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A:Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding an acid
A:Reference number: S51588; MUID:95115667
A:Accession: S51589
A:Molecule type: mRNA
A:Cross-references: EMBL:L19342; NID:g437018; PIDN:AAA64995.1; PID:g767828
C:Genetics:
A:Gene: pcht28
A:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-253/Product: chitinase #status predicted <MAT>
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 60.8%; Score 828.5; DB 2; Length 253;
Best Local Similarity 61.6%; Pred. No. 1.4e-64;
Matches 157; Conservative 32; Mismatches 59; Indels 7; Gaps 3;

QY 3 RFAALVCAALLVAAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIA 62
Db 2 KENIVSPVALSCLFLTLTGAQAGSIYTRFLFEQMLSFRRNDACAPARGFYTYDAFIA 61

QY 63 AANTFPGFTGSADDIKRLAFAFGTSHETGTGTRGAADQFQWGYCFKEEISKATSP 122
Db 62 AANSFPGFTGGDDTARKKETAFAFGTSHETKGSAGT---FTGGYCFYRQIDQ--SDR 116

QY 123 YYGRGPIQLTGRSNYDLAAGRAI--GKDIYNSPDLVSTDAVVSFRTAMFWMTAOGNKPSC 180
Db 117 YYGRGPIQLTGRSNYERAGGIGVGODLVNPNLVAIDPIISFRTAIFWMTAOGNKPSC 176

QY 181 HNVALRRWTPTAADTAAGRPVGVITNIINGLEGCMGRNDANVDRIYTRYCYGMLGT 240
Db 177 HNVIIQGWTPSPADTAANRPVGVITNIINGLEGCMGMPENTAVESRIGFYRRYCGMLNV 236

QY 241 ATGGNLDCYTORNFA 255
Db 237 PTGENLDCNNQKNEA 251

RESULT 7
S20737
Chitinase (EC 3.2.1.14) PR-P - common tobacco
N:Alternate names: acidic chitinase PR-P
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S20737
R:Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meu
submitted to the EMBL Data Library, January 1990
A:Description: Constitutive expression of acidic and basic Chitinase in transgenic to
A:Reference number: S20737
A:Accession: S20737
A:Molecule type: mRNA
A:Residues: 1-253 <LIN>
A:Cross-references: EMBL:X51426; NID:g19770; PIDN:CAA35790.1; PID:g19771
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 60.0%; Score 817.5; DB 2; Length 253;
Best Local Similarity 61.4%; Pred. No. 1.2e-63;
Matches 153; Conservative 34; Mismatches 55; Indels 7; Gaps 3;

QY 7 LAVCAAAALLVAAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANT 66
Db 10 LPCCVFFFLFLT---GSLAQGIGSVITNDLFNEMLKRNDRGCPANGFYTYDAFIAAANS 65

QY 67 PFGFGTGSADDIKRLAFAFGTSHETGTGTRGAADQFQWGYCFKEEISKATSPPYGR 126
Db 66 PFGFGTSGDDTARKKETAFAFGTSHETGTGSL-SAEPTGGYCFVQRNDQ--SDRYGR 122

QY 127 GPIQLTGRSNYDLAAGRAIGKDIYNSPDLVSTDAVVSFRTAMFWMTAOGNKPCHNVALR 186
Db 123 GPIQLTGNQNYEKAGNAIRQDILVNNPDLVAIDTISFKTAIFWMTAOGNKPCHNVALR 182

QY 187 RWTPTAADTAAGRPVGVITNIINGLEGCMGRNDANVDRIYTRYCYGMLGTATGNL 246
Db 183 SWTPSAADASANRQPGYGVITNIINGLEGCMGRNDANVDRIYTRYCYGMLGTATGNL 242

QY 247 DCYTORNFA 255
Db 243 DCYNNQORNEA 251

RESULT 8
S51588
Chitinase (EC 3.2.1.14) pcht1 precursor - Lycopersicon chilense (fragment)
N:Alternate names: endochitinase pcht1
C:Species: Lycopersicon chilense
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 22-Jun-1999
C:Accession: S51588
R:Chen, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A:Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding an a
A:Reference number: S51588; MUID:95115667
A:Accession: S51588
A:Molecule type: mRNA
A:Residues: 1-250 <CHE>

a: Cross-references: EMBL:M57210; NID:G310936; PIDN:AAA64998.1; PID:G767827

a: Genes: *chitinase*

a: Gene family: plant chitinase: plant chitinase homology

a: Keywords: glycosidase; hydrolase

a: 1-21 Domain: signal sequence (fragment) #status predicted <SIG>

a: 22-250 Product: chitinase #status predicted <MAT>

a: 231-248 Domain: plant chitinase homology <PCH>

Query Match	59.98;	Score	816.5;	DB 2;	Length	250;	
Best Local Similarity	62.3%;	Pred. No.	1.5e-63;				
Matches	154;	Conservative	30;	Mismatches	56;	Indels	7;
Gaps							
Qy	11	AAALLVAAGAAQAQGVSVITRSVYASMLFRNDSLCPARGFYTYDAFIAAANFPFG	70				
Db	7	ALSCFLFFLELTGTLAQNAGSVITRELFQQLSERNDACPAKGFTYTYDAFIAAANSFPFG	66				
Qy	71	GITGSADDIKDLAAFFQGTSHETTGTFGGAADQFQWGCERKEISKATSPYYRGGP	130				
Db	67	GTTGGDGTARKKEIAAFFQGTSHETNGSGAGT--FTGGYCFVRQDQ--SDRYRGGP	121				
Qy	131	LTGRSNYDLAGRAI--GKDLVSNPLVSTDAVVSFTAMTWMTAQGNKPSCHNYALRR	188				
Db	122	LTHOSYBERAGGIGVGQDLVNNPLVATDPIISFKTAIFWMTAHHNKPSCHNVIIGQW	181				
Qy	189	PTAADTAAGRVPGYCVITNIINGLEGCGMGNDANVDRIGYTYCYGMLGTATGNDLC	248				
Db	182	FTSPADTAANRVPGYGVITNIINGLEGCMGNPTAVESRIGFYRYCGMLNVPTGENLDC	241				
Qy	249	YTORNFA	255				
Db	242	NNCKNFA	248				

RESULT 9

S20741

chitinase (EC 3.2.1.14) - garden petunia

N:Alternate names: acidic chitinase

C:Species: Petunia x hybrida (garden petunia)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999

C:Accession: S20741

R:Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meulster

A:Description: Constitutive expression of acidic and basic Chitinase in transgenic tobacco

A:Reference number: S20737

A:Accession: S20741

A:Molecule type: mRNA

A:Residues: 1-254 <IN>

A:Cross-references: EMBL:X51427; NID:g20503; PIDN:CAA35791.1; PID:g20504

C:Superfamily: plant chitinase; plant chitinase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:29-252/Domain: plant chitinase homology <PCH>

Query Match	59.8%;	Score 814.5;	DB 2;	Length 254;
Best Local Similarity	62.1%;	Pred.No. 2.3e-63;		
Matches 154; Conservative 31; Mismatches 62; Indels 1; Gaps 1;				
<hr/>				
QY	8	AVCAAAALLVAAAGGAAAGVGSVITRSYASMLPNRDNLSLPCARFGFTYDFAIAAANTF	67	
Dd	6	SVLALSFWVFLLTIGLAQNQSGIVTSIDLFQDMKLRNDARCFAVRFTYDFAIAAANSE	65	
<hr/>				
QY	68	PGRTGTGSADDIKRDIAAFGGTSHETTGTRGAADQFQWGYCFEETSKA [*] SPPIYGKG	127	
Dd	66	PGFTIGDDTARKKEIAAFGGQTSHETTGGTLSPDPYAGGYCFLRE-GNQMGNGYYGEG	124	
<hr/>				
QY	128	PIQLGRSNYDLAAGRAIGKDLYSNPDLVSTDAVVSPRTAMFWMTAQGNKPCHNVALNR	187	
Dd	125	PIQLTQSNNYDLAKGATEQDLVNPNPLVDATVSFKTAIFWMTPGQNKPSCHDVITGR	184	
<hr/>				
QY	188	WTPTAADTAAGRPVPGCVTININGGLECGMGRNDAWDRIGVITYRCGLGTATGGNLD	247	

Db 185 WTPSAOTSANRPGYGVYIINLINGIECGKGQARVEDRIGYRRNVSMNVAPGDNLD 244

Qy 248 CYTQRNFA 255
|| |||||

Db 245 CYNQRNFA 252

RESULT 10

T03017

probable chitinase (BC 3.2.1.14) class II - rice (fragment)

N:Alternate names: class II acidic chitinase; Rcht2

C:Species: Oryza sativa (rice)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C:Accession: T03017

R:Kim, C.Y.; Gal, S.W.; Choe, M.S.; Jeong, S.Y.; Lee, S.I.; Cheong, Y.H.; Lee, S.H.;

plant Mol. Biol. 37, 523-534, 1998

A:title: A new class II rice chitinase, Rcht2, whose induction by fungal elicitor is

A:Reference number: 214820; MIMD:98278381

A:Accession: T03017

A>Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: mRNA

A:Residues: 1-175 <KIM>

A:Cross-references: EMBL:L40338; NID:g2340042; PIDN:AAC37516.1; PID:g2340043

A:Experimental source: cv. Cheongcheongbyeol

C:Function:

A:Description: catalyzes the hydrolysis of the beta-1,4-N-acetyl-D-glucosamine linkage

C:Keywords: glycosidase; hydrolase

	Query Match	59.8%;	Score 814;	DB 2;	Length 175;
	Best Local Similarity	83.4%;	pred. No. 1.7e-63;		
	Matches 146;	Conservative 13;	Mismatches 16;	Indels 0;	Gaps 0;
QY	82	DLAAFFGQTSHTTGGTTCGAADQFOWGCFKEEISKATSPPYGGRGPIQLTRGNIDLAG	141		
DB	1	ELAAFFGQTSHTTGGTTCGSSDQFOWGCFKEEINKATSPPYGGRGPIQLTGSSNYQAAG	60		
QY	142	RAIGKDLVSNPLDVTDAVVSPTAMFWMTAQGNKPSCHNVALRRWTTPTAADTAAGSRVP	201		
DB	61	NALGDLVLGNPLDVTDAVVSFKTALFWMTAQGNKPSCHVDVLGRWTPSAADTAAYRVP	120		
QY	202	GYGVTTNIINGLEGGMGRNDANVRDRIGYITRYCYGMLGTATGNNLDCYQNRNAS	256		

RESULT 11

A34801
pathogenesis-related protein P precursor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C:Accession: A34801
R:Payne, G.; Ahn, P.; Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A:Title: Isolation of complementary DNA clones encoding pathogenesis-related proteins
A:Reference number: A34801; MUID:90115914
A:Accession: A34801
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <P>
A:Cross-references: GB:M29869; NID:g170311; PIDN:AAA34106.1; PID:g170312
C:Superfamily: plant chitinase; plant chitinase homology
g:30-251/Domain: plant chitinase homology <PCH>

```

Query Match          59.4%; Score 808.5; DB 2; Length 253;
Best local similarity 61.0%; Pred. No. 7.5e-63;
Matches 152; Conservative 34; Mismatches 56; Indels 7; Gaps 3;

QY 7 LACAAALILAAAGAAAGAGVGSVITRSYASMLNPNRDNLCSPARGFTYDAFTAAANT 66
10 LKCVCFEFTT---GSIACGTSISVTNDINFMILKNRNDGCPANGFTYDAFTAAANS 65

```

Query Match	58.6%;	Score 797.5;	DB 2;	Length 340;
Best Local Similarity	50.3%;	Pred. No. 9.4e-62;		
Matches 162; Conservative	28;	Mismatches 61;	Indels 71;	Gaps 5;

```

Db 74 CGPTPTPPSPSDGVSIVPRDLFERLLHRNDGACPARGFYTYEAFIAAAAFPAFG 133
QY 73 TGSADDIKRLAAPPFGTSHETTTGTRGAAD-QFQWGYCFKKEISKATSP----- 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 TGNTEKREVAALFGTSHETTTGWTAPDGPFSWGYCFKQE-----QNPPSDYQPSPE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 -----YGRGPIQLTGRSNYDLAIGRAIGKDLVSNPDVSTDAVYFRTAMFWMTAQ 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 WPCAPGRKYYGRGPIQLSFNFNYGAGRAIGVDLLSNPDVATDATVSKTALWFMWTFQ 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 GNKPSCHNVALRRWTPAADAAGRGVGYVTININGLEGCGMRDNDVDRIGYTYRY 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 GNKPSSSHVITGRWAPSPADAAGRAPGYGVITINVGLEGCGHPDPRVANRIGFYQRY 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 CGMLGTATGNGNLCYTQNFAS 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 310 CGAFGIGTGGNLCYNQRPENS 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
S39979
C:Species: Oryza sativa (rice)
C:Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S39979
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice ch
A:Reference number: S39979; MUID:94049667
A:Accession: S39979
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <NIS>
A:Cross-references: EMBL:X56787
A:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:91-329/Domain: plant chitinase homology <PCH>

Query Match 58.4%; Score 795; DB 2; Length 339;
Best Local Similarity 50.8%; Pred. No. 1.5e-61;
Matches 161; Conservative 28; Mismatches 58; Indels 70; Gaps 5;

QY 6 ALAVCAAAALLA-----VARGGA----- 23
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 ALAVLAALATARAECGAAGARCPNCLCSRNGWCGTTSDFCGDCGQCSCGCGPT 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 24 -----AAQGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANTPPGFTGTSAD 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 TPTPPSPSDGVSIVPRDLFERLLHRNDGACPARGFYTYEAFIAAAAFPAFGTGNTE 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 DIRDLAAPPFGTSHETTTGTRGAAD-QFQWGYCFKKEISKATSP----- 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 TRKREVAALFGTSHETTTGWTAPDGPFSWGYCFKQE-----QNPPSDYQPSPEWPCAP 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 ---YGRGPIQLTGRSNYDLAIGRAIGKDLVSNPDVSTDAVYFRTAMFWMTAQGNKPS 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 GRKYIGRPIQLSFNFNYGAGRAIGVDLLSNPDVATDATVSKTALWFMWTFQGNKPS 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 CHNYALRRWTPAADAAGRGVGYVTININGLEGCGMRDNDVDRIGYTYRYCGMLG 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 SHDVITGRWAPSPADAAGRAPGYGVITINVGLEGCGHPDPRVANRIGFYQRYCGAFG 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 TATGGNLDCYTQNFAS 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 TGTGNLDCYNQRPENS 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 18:33:16 ; Search time 78.59 seconds
(without alignments)
119.432 Million cell updates/sec

Title: US-09-534-229C-1

Perfect score: 1362

Sequence: 1 MARFAALAVCAALLAVAA.....MLGTATGGLDCTQRFAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	854.5	62.7	253	1	CHI_Q_TOBAC
2	850	62.4	247	1	CHI_B_LYCES
3	828.5	60.8	253	1	CHIA_LYCCI
4	814.5	59.8	254	1	CHIT_PETHY
5	808.5	59.4	253	1	CHIP_TOBAC
6	803.5	59.0	253	1	CHIA_LYCES
7	772	56.7	266	1	CHI2_HORVU
8	768	56.4	322	1	CHI2_BRANA
9	754.5	55.4	318	1	CHI1_HORVU
10	751	55.1	322	1	CHIT_ARYTH
11	747.5	54.9	336	1	CHI2_ORYSA
12	739.5	54.3	314	1	CHIB_VITVI
13	723	53.1	320	1	CHIX_PEA
14	723	53.1	324	1	CHI1_GOSHI
15	721.5	53.0	318	1	CHI1_ORYSA
16	718.5	52.8	328	1	CHIT_PHAVU
17	718	52.7	321	1	CHI1_THECC
18	711.5	52.2	327	1	CHI5_PHAVU
19	711	52.2	302	1	CHI2_GOSHI
20	709	52.1	328	1	CHIT_SOLU
21	708	52.0	334	1	CHI3_TOBAC
22	705.5	51.8	324	1	CHI2_TOBAC
23	705	51.8	316	1	CHI2_SOLU
24	705	51.8	318	1	CHI1_SOLU
25	701	51.5	329	1	CHI1_TOBAC
26	699	51.3	318	1	CHI3_SOLU
27	699	51.3	324	1	CHI2_PEA
28	692	50.8	322	1	CHTC_LYCES
29	670	49.2	246	1	CHID_LYCES
30	663.5	48.7	340	1	CH16_POPTR
31	644.5	47.3	302	1	CH14_SOLU
32	614	45.1	303	1	CH1A_POPTR
33	566.5	41.6	316	1	CHI8_POPTR

ALIGNMENTS

RESULT 1
CHI_Q_TOBAC STANDARD; PRT; 253 AA.
AC P17514;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ACIDIC ENDOCHITINASE Q PRECURSOR (EC 3.2.1.14) (PATHOGENESIS-RELATED PROTEIN Q) (PR-Q).

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4097;

RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=CV. XANTHI NC;

RA MEDLINE=90115914; PubMed=2296608;

RA Payne G., Ahl P., Moyer M., Harper A., Beck J., Meins F. Jr.,

RA Ryals J.;

RT "Isolation of complementary DNA clones encoding pathogenesis-related proteins P and Q, two acidic chitinases from tobacco.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:98-102(1990).

[2]
SEQUENCE FROM N.A.

RC STRAIN=CV. SAMSUN; TISSUE=Leaf;

RA MEDLINE=92033079; PubMed=2131096;

RA Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,

RA Bol J.F., van Roekel J., Meulenhof J., Cornelissen B.J.C.;

RA "Analysis of acidic and basic chitinases from tobacco and petunia and their constitutive expression in transgenic tobacco.";

RT Mol. Plant Microbe Interact. 3:252-258(1990).

RL CHITIN CONTAINING FUNGAL PATHOGENS.

CC -!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST

CC CHITIN CONTAINING FUNGAL PATHOGENS.

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF

CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR FLUID FROM LEAVES.

CC -!- INDUCTION: DURING LOCAL NECROTIC RESPONSE TO THE TOBACCO MOSAIC

CC VIRUS.

CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO

CC CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-

CC BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL

CC HYDROLASES).

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CC EMBL; M29868; AAA34107.1; -

DR EMBL; X51425; CAA35789.1; -

DR PIR; B34801; B34801.

DR PIR; S20738; S20738.

DR

DR


```

Db 2 KFNIVSPVALSCFLFELTGTILAOAGSIVITRELEQMLSPFNDDACPAKGYFYDARIA 61
QY 63 AANTPPGFGTGSADDIRDLAAAFQGTSHETTGRTGAADQFQWGYCFKKEISKATPPP 122
Db 62 AANSPPGFGTAGDDTARKKEIAAPFGQTSHTNGSGAGT--FTGGYCFVKQIEQ--SDR 116
QY 123 YGGRPIQLTGRSNYDLAAGRAI--GKDLVSNPDLYSTDAVVSFRTAMFWMTAOGNKPSC 180
Db 117 YGGRPIQLTHQSNYERAGOGVGQELVNNPDILVATDPIISFKTAIFWMTQDNKPSC 176
QY 181 HNVALLRRTPTAADAAGRVPGYGVYITNIINGLEGCGMRDANDVDRIGYTRYCGMLGT 240
Db 177 HNVITGQWTPSPKDAANRVPGYGVYITNIINGLEGCGMPNTAAESRIGFYRKYCGMLNV 236
QY 241 ATGGNLDCTYQRNFA 255
Db 237 PTGENLDCNNQKNFA 251

RESULT 7
ID CH12_HORVU STANDARD; PRT; 266 AA.
AC P23951;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 26 KDA ENDOCHITINASE.2 PRECURSOR (EC 3.2.1.14) (CHI-26).
OS Hordeum vulgare (barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=CV. PIGGY;
RX MEDLINE=91107649; PubMed=1899089;
RA Leah R., Tommerup H., Svendsen I., Mundy J.;
RT "Biochemical and molecular characterization of three barley seed
RT proteins with antifungal properties.";
RL J. Biol. Chem. 266:1564-1573(1991).
RN [2]
RP PRELIMINARY SEQUENCE OF 24-77 AND 148-188.
RC TISSUE=Endosperm;
RA Leah R., Mikkelsen J.D., Mundy J., Svendsen I.;
RT "Identification of a 28,000 dalton endochitinase in barley
RT endosperm.";
RL Carlsberg Res. Commun. 52:31-37(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RC TISSUE=Seed;
RX MEDLINE=93132784; PubMed=8421299;
RA Hart P.J., Monzingo A.F., Ready M.P., Ernst S.R., Robertus J.D.;
RT "Crystal structure of an endochitinase from Hordeum vulgare L.
RT seeds.";
RL J. Mol. Biol. 229:189-193(1993).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO
CC CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-
CC BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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DR EMBL; L34210; AAA56786.1; -.
DR EMBL; M62904; AAA32941.1; -.
DR PIR; A29104; A29104.
DR PIR; A38664; A38664.
DR PDB; 2BAA; 15-JAN-96.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 266 26 KDA ENDOCHITINASE 2.
FT DISULFID 46 108
FT DISULFID 120 128
FT DISULFID 227 259
FT VARIANT 205 205
FT CONFLICT 173 173
FT CONFLICT 205 205
FT TURN 26 28
FT TURN 31 37
FT TURN 38 42
FT TURN 45 46
FT TURN 49 51
FT TURN 54 62
FT TURN 63 63
FT TURN 65 68
FT TURN 72 73
FT TURN 74 90
FT TURN 91 91
FT TURN 96 97
FT TURN 99 100
FT TURN 102 104
FT STRAND 111 111
FT TURN 130 131
FT STRAND 135 137
FT TURN 138 141
FT STRAND 142 143
FT TURN 145 155
FT TURN 156 156
FT TURN 164 164
FT TURN 165 168
FT TURN 170 187
FT TURN 186 187
FT TURN 191 194
FT TURN 195 197
FT TURN 203 206
FT TURN 207 209
FT TURN 214 222
FT TURN 223 224
FT TURN 233 249
FT TURN 250 250
FT TURN 260 261
FT TURN 266 266
FT TURN 266 AA; 28155 MW; 0949BE88CC20B664 CRC64;
SQ SEQUENCE 266 AA; 28155 MW; 0949BE88CC20B664 CRC64;

Query Match 56.7%; Score 772; DB 1; Length 266;
Best Local Similarity 56.8%; Pred. No. 2.8e-57;
Matches 150; Conservative 31; Mismatches 59; Indels 14; Gaps 2;

QY 6 ALAVCAAAALLAVAGAAAGQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAAN 65
Db 3 SLAVVAVVAIVAMAIGTARGSVSVISRAQFDRLMLHRNDGACQAKGFYTYDAFVAAAA 62
QY 66 TPGFGTTGSADDIRDLAAAFQGTSHETTGRTGAAD-QFQWGYCFKKEISK----- 117
Db 63 APPFGTTGSADAQKREVAALFAQTSHETTGRTGAADPGAFAGWGYCFKKEERASSDYCTP 122
QY 118 -----ATSPPYGGRPIQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWFM 171
Db 123 SAQWPCAPGKRYGGRPIQLTHQSNYERAGOGVGQELVNNPDILVATDPIISFKTAIFWMT 182
QY 172 TAQGNKPSCHNVALLRRTPTAADAAGRVPGYGVYITNIINGLEGCGMRDANDVDRIGY 231

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DR SMART: SM00270; ChtBD1; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 318 26 KDA ENDOCHITINASE 1.
FT DOMAIN 20 62 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 22 37 BY SIMILARITY.
FT DISULFID 31 43 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 53 57 BY SIMILARITY.
SQ SEQUENCE 318 AA; 33402 MW; 42D62B2FE8041954 CRC64;

Query Match 55.4%; Score 754.5; DB 1; Length 318;
Best Local Similarity 48.1%; Pred. No. 9.5e-56;
Matches 153; Conservative 31; Mismatches 71; Indels 63; Gaps 4;

QY 1 MARFAALAVCAALLLAVA-----AGGAAQ----- 26
DB 1 MRAFLVFAVVAATAATVAVAEQCSQAGGATCPNCLCCSRFGWCGSTPYCGDGCSQCSGC 60

QY 27 -----GVGSITRSVYASMLPNRDNLSCLPARGFYTYDAFTAAANTPPGFG 71
DB 61 GGSGTPVTPTPSGGGVSSIVSRALFDRLHRNDGACQAKGFYTYDAFAAASAFRGFG 120

QY 72 TTGSADDIKDLAFAFGQTSHETGTGRGAAD-QFQWGYCFKKEISK----- 117
DB 121 TTGTGTDTRKREVAFLAQTSHETGTGWATPDGAFAGFYCFKQERGATSNYCTPSAQMPC 180

QY 118 ATSPYYVGRPIQLTGRSNYDLAAGTKGLVSNPDVSTDAVVSFRTAMFWMTAGGNK 177
DB 181 APKSYTGGRPIQLSHYNYGPAAGALGVLLRNPDVATDPTVSFTAMWFWMTAQAAPK 240

QY 178 PSCHNVALRRWTTPAADAAGRVPGYGVITNINGLGECGRNDANVDRIGYTRYCGM 237
DB 241 PSSHAVITGQWSPGSDRAAGRVPGFYGVITNINGLGECGRNDANVDRIGYTRYCGM 300

QY 238 LGTATGNLDCYTORNFA 255
DB 301 LGVGYGNLDCYSQRPEFA 318

RESULT 10
CHIT_ARATH STANDARD; PRT; 322 AA.
ID CHIT_ARATH
AC P19171;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN MQC3.32.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sanac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
RT "Isolation and characterization of the genes encoding basic and
RT acidic chitinase in Arabidopsis thaliana.";
RL Plant Physiol. 93:907-914(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 pl, TAC
RT and BAC clones.";
```

```

RL DNA Res. 7:217-221(2000).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSES OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -!- TISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL IN ROOTS WITH LOWER
CC LEVELS IN LEAVES AND FLOWERING SHOOTS.
CC -!- INDUCTION: ETHYLENE INDUCES HIGH LEVELS OF SYSTEMIC EXPRESSION
CC OF BASIC CHITINASE WITH EXPRESSION INCREASING WITH PLANT AGE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH INCLUDE A N-TERMINAL
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC
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CC
CC EMBL: M38240; AAA32769.1; ALT_INIT.
CC EMBL: AF002047; BAB03157.1; -.
CC HSSP: P23951; 2BAA.
CC InterPro: IPR001002; Chitin_bind.
CC DR InterPro: IPR000726; Glyco_hydro_19.
CC DR Pfam: PF00187; Chitin_binding_1.
CC DR Pfam: PF00182; Glyco_hydro_19; 1.
CC DR PRINTS: PR00451; CHITINBINDNG.
CC DR PRODOM: PD000574; Glyco_hydro_19; 1.
CC DR PRODOM: PD000609; Chitin_bind; 1.
CC DR SMART: SM00270; ChtBD1; 1.
CC DR PROSITE: PS00026; CHITIN_BINDING; 1.
CC DR PROSITE: PS00773; CHITINASE_19_1; 1.
CC DR PROSITE: PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
FT SIGNAL 1 20
FT CHAIN 21 315 BASIC ENDOCHITINASE.
FT PROPEP 316 322 REMOVED IN MATURE FORM (PROBABLE).
FT DOMAIN 21 63 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 322 AA; 34609 MW; C9AFFE4C544FCCD7 CRC64;
```

```

Query Match 55.1%; Score 751; DB 1; Length 322;
Best Local Similarity 56.8%; Pred. No. 1.9e-55;
Matches 138; Conservative 35; Mismatches 56; Indels 14; Gaps 2;

QY 28 VGSVITRSVYASMLPNRDNLSCLPARGFYTYDAFTAAANTPPGFTGSGADDIKDLAAFF 87
DB 73 USGIISSQFDDMLKRRNDACPARGFYTYDAFTAAANTPPGFTGDTATRKKEVAFF 132

QY 88 GQTSHTTGGTGAAD-QFQWGYCFKKEISK-----ATSPYYGGRGPIQLTG 133
DB 133 GQTSHTTGGWATPDGYPYSGWGYCFKQEQNPASDYCEPSATWPCASGKRYGPGMQLSW 192

QY 134 RSNYDLAAGIKDLVSNPDVSTDAVVSFRTAMFWMTAOGNKPSCHNVALRRWTPTAA 193
DB 193 NNYNYGLCGRAIGVDLLNPDVANDAVIAFAKAAIWFMTAOGPKPSCHAVIAGQWPSDA 252

QY 194 DTAAGRVPGYGVITNINGLGECGRNDANVDRIGYTRYCGMLGTATGGLDCTYORN 253
DB 253 DRAAGRLPGYGVITNINGLGECGRGDGRVADRIFYQRYCNYFVNPVGNLDCYNQRS 312

QY 254 FAS 256
DB 313 FVN 315
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Db 250 TQWTPSADQORAGRVPGYGVITNIINGGLECGHEDDRIADIGFYKRYCDILGVSYGA 309
QY 245 NLDYTOR 252
Db 310 NLDYSQR 317
RESULT 12
CHIB_VITVI STANDARD; PRT; 314 AA.
ID CHIB_VITVI AC P51613;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CHIT1B.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PINOT;
RX MEDLINE=98052138; PubMed=9390436;
RA Busam G., Kassemeyer H.H., Matern U.;
RT "Differential expression of chitinases in Vitis vinifera L.
RT responding to systemic acquired resistance activators or fungal
RT challenge.";
RL Plant Physiol. 115:1029-1038(1997).
CC -!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; 254234; CAA90970.1; -
CC HSP; P23951; 2BAA.
DR InterPro: IPR001002; Chitin_bind.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam: PF00187; chitin_binding; 1.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR PRINTS: PR00451; CHITINBINDING.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR ProDom: PD000609; Chitin_bind; 1.
DR SMART: SM00270; ChtBd1; 1.
DR PROSITE: PS00026; CHITIN_BINDING; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 314 BASIC ENDOCHITINASE.
FT DOMAIN 21 61 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 55 59 BY SIMILARITY.
SQ SEQUENCE 314 AA; 33429 MW; 3802484ED69BC6C0 CRC64;

Query Match 54.3%; Score 739.5; DB 1; Length 314;
Best Local Similarity 48.2%; Pred. No. 1.7e-54;

Db 250 TQWTPSADQORAGRVPGYGVITNIINGGLECGHEDDRIADIGFYKRYCDILGVSYGA 309
QY 245 NLDYTOR 252
Db 310 NLDYSQR 317
RESULT 11
CH2_ORYSA STANDARD; PRT; 336 AA.
ID CH2_ORYSA AC P25765;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).
GN RCH10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91238706; PubMed=2034221;
RA Zhu Q., Lamb C.J.;
RT "Isolation and characterization of a rice gene encoding a basic
RT chitinase.";
RL Mol. Gen. Genet. 236:289-296(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC PIR; S15997; S15997.
DR HSP; P23951; 2BAA.
DR InterPro: IPR001002; Chitin_bind.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam: PF00187; chitin_binding; 1.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR PRINTS: PR00451; CHITINBINDING.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR ProDom: PD000609; Chitin_bind; 1.
DR SMART: SM00270; ChtBd1; 1.
DR PROSITE: PS00026; CHITIN_BINDING; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 336 BASIC ENDOCHITINASE 2.
FT DOMAIN 22 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 24 39 BY SIMILARITY.
FT DISULFID 33 45 BY SIMILARITY.
FT DISULFID 38 52 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 336 AA; 35565 MW; 7F4EC126265DEA84 CRC64;

Query Match 54.9%; Score 747.5; DB 1; Length 336;
Best Local Similarity 57.3%; Pred. No. 3.8e-55;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGSAAAGGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAANTFPGFTGSGADDI 79
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 ASGGGGGCVASIVSRSLFDMLLRNDACPASNFYDFAVAASAFPGFAAGDADTN 129
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 KRDLAAFGQTSHTTGGTGAAD-QFQWGYCPEKEELSK-----ATSPPY 124
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 KREVAAPFACHTSHETGGWATADPGYTWGFCFKEENGAGPDYCCQSAOWPCPAAGKKY 189
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 125 GRGPIQLTGRSNYDLAGRAIGKDLVSNPDLYSTDAVYSFRTAMFWMTAQNPKPSCHNVA 184
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 GRGPIQLSYNENYCPAGCATGADLLGPDPLVASDATYSFDTAFWMTQSPKPKSCNAVA 249
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
+ + + + + : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 185 LRRWTPTAADTAAGRVPGYGVITNIINGGLECGMRNDANVDRIGYTRYCGMLGTATGG 244
+ + + + + : : : : + + + + + + + + + + + + + + + + + + + + + + + + + + +
+ + + + + : : : : + + + + + + + + + + + + + + + + + + + + + + + + + + +
```


us-09-534-229c-1.rsp

Tue May 7 10:52:13 2002

Search completed: May 3, 2002, 18:48:31
Job time: 915 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: May 3, 2002, 18:32:16 ; Search time 157.87 Seconds
(without alignments)
237.193 Million cell updates/sec

Title: US-09-534-229C-1
Perfect score: 1362
Sequence: 1 MARFAALAVCAALLLAVAA.....MLGATGGLDCYTQRFAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_17:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1334	97.9	256	Q43764	Q43764 hordeum vul
2	1277	93.8	252	Q9AX88	Q9AX88 secale cere
3	1266	93.0	252	Q43765	Q43765 hordeum vul
4	1139.5	83.7	261	Q9FW99	Q9FW99 oryza sativ
5	1128.5	82.9	261	O80423	O80423 oryza sativ
6	1128	82.8	249	Q9LEH7	Q9LEH7 hordeum vul
7	1000	73.4	296	Q9FWE7	Q9FWE7 oryza sativ
8	973.5	71.5	289	O04271	O04271 oryza sativ
9	825.5	60.6	236	Q43835	Q43835 solanum tub
10	822.5	60.4	251	Q9SBJ9	Q9SBJ9 solanum tub
11	822.5	60.4	252	Q43834	Q43834 solanum tub
12	819.5	60.2	240	O22568	O22568 solanum tub
13	814	59.8	175	O24007	O24007 oryza sativ
14	808.5	59.4	253	O82552	O82552 capsicum an
15	805.5	59.1	264	Q42515	Q42515 arachis hyp
16	797.5	58.6	340	Q43294	Q43294 oryza sativ
17	772.5	56.7	332	Q42839	Q42839 hordeum vul
18	768	56.4	266	Q9FRV0	Q9FRV0 secale cere
19	767	56.3	335	Q9SXJ1	Q9SXJ1 arabis gemm

20	764	56.1	320	10	Q9M7G7	Q9m7g7 arabis glab
21	763	56.0	321	10	Q9FRV1	Q9frv1 secale cere
22	760.5	55.8	260	10	Q9FPM1	Q9fpm1 fragaria an
23	758.5	55.7	320	10	Q42994	Q42994 oryza sativ
24	758	55.7	299	10	Q9M7H7	Q9m7h7 arabis holb
25	758	55.7	300	10	Q9M7H1	Q9m7h1 arabis fecu
26	758	55.7	323	10	Q42993	Q42993 oryza sativ
27	757	55.6	294	10	Q9M7F6	Q9m7f6 arabis micr
28	757	55.6	326	10	P93680	P93680 persea amer
29	756.5	55.5	311	10	O80404	O80404 cucurbita m
30	756	55.5	302	10	Q9M7G4	Q9m7g4 arabis lemm
31	755	55.4	300	10	Q9M7G1	Q9m7g1 arabis lign
32	754	55.4	305	10	Q9M7H2	Q9m7h2 arabis drum
33	754	55.4	312	10	Q9M7F5	Q9m7f5 arabis pari
34	753.5	55.3	308	10	Q9M7H4	Q9m7h4 arabis blep
35	753	55.3	326	10	Q9M7H0	Q9m7h0 arabis fecu
36	753	55.3	333	10	Q42992	Q42992 oryza sativ
37	752	55.2	295	10	Q9M7G0	Q9m7g0 arabis lign
38	752	55.2	295	10	Q9M7F7	Q9m7f7 arabis micr
39	752	55.2	306	10	Q9M7G2	Q9m7g2 arabis lign
40	751	55.1	335	10	Q9SXJ4	Q9sxj4 arabidopsis
41	751	55.1	335	10	Q9S7J5	Q9s7j5 arabidopsis
42	751	55.1	335	10	Q9S838	Q9s838 arabidopsis
43	750	55.1	312	10	Q9M7F4	Q9m7f4 arabis pari
44	749	55.0	310	10	Q9M7G9	Q9m7g9 arabis glab
45	749	55.0	335	10	Q9SXJ2	Q9sxj2 arabidopsis

ALIGNMENTS

RESULT 1

Q43764	Q43764	PRELIMINARY;	PRT;	256 AA.
ID	Q43764;			
AC	Q43764;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).			
DE	ACETYLGLUCOSAMINIDASE (Barley).			
GN	CHIA0 OR CHT2A.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_taxonomy:4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. PALLAS, NEAR-ISOGENIC LINE P02; TISSUE=LEAF;			
RA	Bryngelsson T., Collinge D.B., Green B., Gummeson P.O., Kragh K.,			
RA	Thordal-Christensen H.;			
RL	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.			
RC	!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-			
CC	ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.			
DR	EMBL; X78671; CAA55344.1; -			
DR	HSSP; P23951; 2BAA.			
DR	Mendel; 24; Horvu;Chia0;24.			
DR	InterPro; IPR000726; Glyco_hydro_19.			
DR	Pfam; PF00182; Glyco_hydro_19; 1.			
DR	ProDom; PD000574; Glyco_hydro_19; 1.			
DR	PROSITE; PS00773; CHITINASE_19; 1.			
DR	PROSITE; PS00774; CHITINASE_19; 2; 1.			
KW	Hydrolase; Glycosidase.			
FT	CHAIN 27 256 CHITINASE.			
SQ	SEQUENCE 256 AA; 27052 MW; FICB619FC5E23FC8 CRC64;			

Query Match 97.9%; Score 1334; DB 10; Length 256;
Best Local Similarity 98.4%; Pred. No. 6.3e-107;
Matches 252; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MARFAALAVCAALLLAVAGGAAAGVGVSIVTSYASMLPRDNLCPARGFYTVDAF 60
|||||

```

Db 1 MARPAALAVCAAAALLLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
QY 61 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 120
Db 61 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 120
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 180
Db 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 180
QY 181 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 240
Db 181 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 240
QY 241 ATGGNLCYTORNFAS 256
Db 241 ATGGNLCYTORNFAS 256

RESULT 2
QYAXR8
ID QYAXR8 PRELIMINARY; PRT; 252 AA.
AC Q9AXR8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 24.8 KDA CLASS II ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=20532799; PubMed=11080301;
RA Yeh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wiseman S.B.,
RA Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.,
RA Lajoie G.;
RT "Chitinase genes responsive to cold encode antifreeze proteins in
RT winter cereals.";
RL Plant Physiol. 124:1251-1264(2000).
DR EMBL; AF280438; AAG53610.1; -.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 252 AA; 26835 MW; FC9D538F49690823 CRC64;
[1]

Query Match 93.8%; Score 1277; DB 10; Length 252;
Best Local Similarity 93.8%; Pred. No. 4.9e-102;
Matches 240; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARPAALAVCAAAALLLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
Db 1 MARPAALAVCAAAALLLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 56
QY 61 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 120
Db 57 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 116
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 180
Db 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 176
QY 181 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 240
Db 177 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 236
QY 241 ATGGNLCYTORNFAS 256
Db 237 ATGGNLCYTORNFAS 252

RESULT 3
QYAXR8
ID QYAXR8 PRELIMINARY; PRT; 252 AA.
AC Q9AXR8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 24.8 KDA CLASS II ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=20532799; PubMed=11080301;
RA Yeh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wiseman S.B.,
RA Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.,
RA Lajoie G.;
RT "Chitinase genes responsive to cold encode antifreeze proteins in
RT winter cereals.";
RL Plant Physiol. 124:1251-1264(2000).
DR EMBL; AF280438; AAG53610.1; -.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 252 AA; 26835 MW; FC9D538F49690823 CRC64;
[1]

Query Match 93.8%; Score 1277; DB 10; Length 252;
Best Local Similarity 93.8%; Pred. No. 4.9e-102;
Matches 240; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARPAALAVCAAAALLLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
Db 1 MARPAALAVCAAAALLLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 56
QY 61 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 120
Db 57 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 116
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 180
Db 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 176
QY 181 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 240
Db 177 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 236
QY 241 ATGGNLCYTORNFAS 256
Db 237 ATGGNLCYTORNFAS 252

RESULT 4
QYAXR8
ID QYAXR8 PRELIMINARY; PRT; 261 AA.
AC Q9AXR8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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Q43765
ID Q43765 PRELIMINARY; PRT; 252 AA.
AC Q43765;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE (EC 3.2.1.14) (CHITODEXININASE) (1,4-BETA-POLY-N-
DE ACTYLGUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHIAO OR CHT2B.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]

SEQUENCE FROM N.A.
STRAIN=CV. PALLAS, NEAR-ISOGONIC LINE P02; TISSUE=LEAF;
RA Bryngelsson T., Collinge D.B., Green B., Gummeson P.O., Kragh K.,
RA Thordal-Christensen H.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X78672; CAA55345.1; -.
DR HSSP; P23951; 2BA.
DR Mendel; 25; Horvu:Chia0:25.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
KW Hydrolase; Glycosidase.
FT CHAIN 23 252 CHITINASE.
FT SEQUENCE 252 AA; 26629 MW; 8A6209D443E8FDD8 CRC64;

Query Match 93.0%; Score 1266; DB 10; Length 252;
Best Local Similarity 93.0%; Pred. No. 4.3e-101;
Matches 238; Conservative 9; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARPAALAVCAAAALLLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
Db 1 MARYAAL-----AALLAVAVGGAAGQGVSVITQSVYASMLPNRDNLSLCPARGFYTYDAF 56
QY 61 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 120
Db 57 TAAANTFPGFTGSADDIKRDLAAFFGQTSHTTGGTRGAADQFQWGYCFKEEISKATS 116
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 180
Db 117 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRFAMFWMTAOGNKPSC 176
QY 181 HNVALLRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 240
Db 177 HDVALGRWTPPTAADTAAGRVPGYGVITNIINGLGCGRNDANVDRIGYTRYCGMLGT 236
QY 241 ATGGNLCYTORNFAS 256
Db 237 ATGGNLCYTORNFAS 252

RESULT 4
QYAXR8
ID QYAXR8 PRELIMINARY; PRT; 261 AA.
AC Q9AXR8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Wisman V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Felblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
RT "Oryza sativa chromosome 10 BAC OSUNB001511 genomic sequence.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC051633; AAG13608.1; -.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
SQ SEQUENCE 261 AA; 27551 MW; 773133E7813DFDBE CRC64;

Query Match 83.7%; Score 1139.5; DB 10; Length 261;
Best Local Similarity 82.7%; Pred. No. 3.2e-90;
Matches 211; Conservative 20; Mismatches 23; Indels 1; Gaps 1;

QY 3 RFALAVCAAAALLLAAVAGAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIA 62
DB 7 RFVQLAACAAASLLAAVAGAGAAAGVGSVITQAVFNSMLPNRNSQCPARGFYTYDAFIA 66

QY 63 AANTFPFGGTT-GSADDIKRDIAAFFGOTSHETGGTRGAADQFOWGYCFKEEISKATSP 121
DB 67 AANSFPAGCTSGGSAELLIRLAAFFGOTSHETGGTRGSSDQFOWGYCFKEEINKATSP 126

QY 122 PYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPSCH 181
DB 127 PYYGRGPQLTGRSNYQAAGNALGLDLVGNEDVSTDAVVSFRTAMFWMTAQGNKPSCH 186

QY 182 NVALLRWPTPTAATTAAGRVPGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGTA 241
DB 187 DVLGRWTPSAADTAAGRVPGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGAG 246

QY 242 TGGNLDCTYQNFAS 256
DB 247 YGSNLDCTYQNFAS 261

RESULT 5
ID O80423 PRELIMINARY; PRT; 261 AA.
AC O80423;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE CHITINASE.
GN CHIAO OR RCHT2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Itch Y., Yamamoto K., Sasaki T.;
RT "Nucleotide sequence of rice acidic class II chitinase OsChia2a.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016497; BAA31997.1; -.
DR HSSP; P23951; 2BAA.
DR Mendel; 31086; Oryza; Chia0:31086.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
FT CHAIN 30 261 CHITINASE IIA.
SQ SEQUENCE 261 AA; 27601 MW; 6760C2578121E0BF CRC64;

Query Match 82.9%; Score 1128.5; DB 10; Length 261;
Best Local Similarity 82.7%; Pred. No. 3.2e-90;
Matches 211; Conservative 20; Mismatches 23; Indels 1; Gaps 1;
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Best Local Similarity 82.0%; Pred. No. 2.9e-89;
Matches 209; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

QY 3 RFALAVCAAAALLLAAVAGAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIA 62
DB 7 RFVQLAACAAASLLAAVAGAGAAAGVGSVITQAVFNSMLPNRNSQCPARGFYTYDAFIA 66

QY 63 AANTFPFGGTT-GSADDIKRDIAAFFGOTSHETGGTRGAADQFOWGYCFKEEISKATSP 121
DB 67 AANSFPAGCTSGGSAELLIRLAAFFGOTSHETGGTRGSSDQFOWGYCFKEEINKATSP 126

QY 122 PYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPSCH 181
DB 127 PYYGRGPQLTGRSNYQAAGNALGLDLVGNEDVSTDAVVSFRTAMFWMTAQGNKPSCH 186

QY 182 NVALLRWPTPTAATTAAGRVPGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGTA 241
DB 187 DVLGRWTPSAADTAAGRVPGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGAG 246

QY 242 TGGNLDCTYQNFAS 256
DB 247 YGSNLDCTYQNFAS 261

RESULT 6
ID Q9LEH7 PRELIMINARY; PRT; 249 AA.
AC Q9LEH7;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE CHITINASE II.
GN CHT2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIDAS.
RA Green R.M., Bevan M.;
RT "Isolation and characterisation of genes induced in barley during
RT powdery mildew infection.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIDAS.
RA Green R.M.;
RL Thesis (1991), University of Cambridge, UK.
DR EMBL; AJ276226; CAB99486.1; -.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
SQ SEQUENCE 249 AA; 27127 MW; ED85AB6E9E6FEB88 CRC64;

Query Match 82.8%; Score 1128; DB 10; Length 249;
Best Local Similarity 93.6%; Pred. No. 3e-89;
Matches 206; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 37 YASMLPNRNSLCPARGFYTYDAFIAAANTFPFGGTTGSADDIKRDIAAFFGOTSHETG 96
DB 30 YASMLPNRNSQCPGQGFYTYVREIAAANTFPFGGTTGSADDIKRDIAAFAFGQSHETG 89

QY 97 GTRGAADQFOWGYCFKEEISKATSPYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDVLS 156
DB 90 GTRGAADQFOWGYCFKEEINKATSPYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDVLS 149

QY 157 TDVVSPTAMFWMTAQGNKPSCHNVALRWPTPTAADTAAGRVPGYGVITNIINGLEG 216
```

Db 150 TDVVVFRTAIFWMTAGNKPSSHDVALGRWTPAATDAGRVPGYGVITNIIINGGLEC 209
 QY 217 GMRGRDANVDRIGYTRCYGMLGATGGLNLCYQTNFAS 256
 Db 210 GMRGRDANVDRIGYTRCYGMLGATGGLNLCYQTNFAS 249

RESULT 7
 Q9FWF7 PRELIMINARY; PRT; 296 AA.
 ID Q9FWF7;
 AC Q9FWF7;
 DT 01-MAR-2001 (TREMREL. 16, Created)
 DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
 DE PUTATIVE CHITINASE.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
 RA Hsiao J., Zisman V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
 RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RA "Oryza sativa chromosome 10 BAC OSNB0015111 genomic sequence.";
 RL Submitted (06-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC051633; AAG13590.1;
 DR InterPro; IPR000726; Glyco_hydro.19.
 DR Pfam; PF00182; Glyco_hydro.19; 2.
 DR ProDom; PD000574; Glyco_hydro.19; 1.
 DR PROSITE; PS00773; CHITINASE_19.1; 1.
 SQ SEQUENCE 296 AA; 32169 MW; 1C0F8158ESCf119B CRC64;

Query Match 73.4%; Score 1000; DB 10; Length 296;
 Best Local Similarity 67.7%; Pred. No. 3.6e-78;
 Matches 195; Conservative 22; Mismatches 33; Indels 38; Gaps 3;

QY 3 RFALAVCAALLLAVAGAAAGVGVITRSVYASMLNPNRNSLCPARGFYTDAFIA 62
 Db 10 RFVLAACAVAVILLAVAGAAAGVGVITAEVFNMLNPNRNSLCPARGFYTDAFIA 69
 QY 63 AANTPEGFTT-GSADIKRDLAFAFFGQTSHETGGTGAADQFQWGYCFKEEISKATSP 121
 Db 70 AANSFPAGTSGGSAELIRLELAFFGQTSHETTDGTRGSSDQFQWGYCFKEEINKATSP 129
 QY 122 PYGPGPIQLTG-----RSNYDLAAGRAIGKDL 148
 Db 130 PYGPGPIQLTGFTIINTYMLNPAISLAVYPIYSINYESHAIELPSSQERAGAPGR-- 187
 QY 149 VSNPDLVSTDAVFRFAMWMTAAGNKPSCNHNALRRWTPAATDAGRVPGYGVITN 208
 Db 188 --RDLVSTNAVSEFKTAIFWMTGQYKNPSSHDVILGRWTPSAADTAAAGRVPGYGVITN 245
 QY 209 IINGLEGCGMRDANVDRIGYTRCYGMLGATGGLNLCYQTNFAS 256
 Db 246 IINGFECDVGQNDANVDRIGYTRCYGMLGADPGSNLDCYNQDFDS 293

RESULT 8
 O04271 PRELIMINARY; PRT; 289 AA.
 ID O04271;
 AC O04271;
 DT 01-JUL-1997 (TREMREL. 04, Created)
 DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
 DE CHITINASE.
 GN CHIAO.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IR36;
 RA Yun C.-H., Lee B.P., Yun K.J., Eun M.Y.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF001500; AAB58238.1; -.
 DR HSSP; P23951; 2BAA.
 DR Mendel; 14790; Oryza; Chia0;14790.
 DR InterPro; IPR000726; Glyco_hydro.19.
 DR Pfam; PF00182; Glyco_hydro.19; 1.
 DR ProDom; PD000574; Glyco_hydro.19; 1.
 DR PROSITE; PS00774; CHITINASE_19.2; 1.
 SQ SEQUENCE 289 AA; 31037 MW; 3EB53DF957B8FE72 CRC64;

Query Match 71.5%; Score 973.5; DB 10; Length 289;
 Best Local Similarity 74.4%; Pred. No. 6.6e-76;
 Matches 186; Conservative 19; Mismatches 38; Indels 7; Gaps 3;

QY 9 VCAA----ALLAVAGAAAGVGVITRSVYASMLNPNRNSLCPARGFYTDAFIAA 64
 Db 38 VCSACRVPAALLAVAAW--RROGVGVITQAVFNMLNPNRNSLCPARGFYTDAFIAA 95
 QY 65 NIFPGFTTGS-ADIKRDLAFAFFGQTSHETGGTGAADQFQWGYCFKEEISKATSP 123
 Db 96 NSFRSARAGGAPSSRRLELAFFGQTSHETGGTGRSSDQFQWGYCFKEEINKATSP 155
 QY 124 YGRGPIQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVFERTAMWMTAAGNKPSCN 183
 Db 156 YGRGPIQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVFERTAMWMTAAGNKPSCN 215
 QY 184 ALRWTPAATDAGRVPGYGVITNIIINGLEGCGMRDANVDRIGYTRCYGMLGATG 243
 Db 216 ILGRWTPGTTAGRVPGYGVITNIIINGLEGCGMRDANVDRIGYTRCYGMLGATG 275
 QY 244 GNLDCTQORN 253
 Db 276 SNLDCTQORN 285

RESULT 9
 Q43835 PRELIMINARY; PRT; 236 AA.
 ID Q43835;
 AC Q43835;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
 DE CLASS II CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
 DE ACTYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE) (FRAGMENT).
 GN CHIAO OR CHPAL.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. DATURA; TISSUE=LEAF;
 RX MEDLINE=9808002; PubMed=9426596;
 RA Buchter R., Stromberg A., Schmelzer E., Kombrink E.;
 RT "Primary structure and expression of acidic (class II) chitinase in
 RT potato.";
 RL Plant Mol. Biol. 35:749-761(1997).
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-

Tue May 7 10:52:14 2002

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RT "A new class II rice chitinase, RcHt2, whose induction by fungal
RT elicitor is abolished by protein phosphatase 1 and 2A inhibitor.";
RL Plant Mol. Biol. 37:523-534(1998).
DR EMBL; L40138; AAC37516.1; -.
DR HSP; P23951; 2BAA.
DR Mendel; 26889; Oryza; Chiao; 26889.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase.
FT NON_TER 1
SQ SEQUENCE 175 AA; 18969 MW; 489333BLBAFCBLFCE CRC64;

Query Match 59.8%; Score 814; DB 10; Length 175;
Best Local Similarity 83.4%; Pred. No. 1.8e-62;
Matches 146; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 82 DIAAFFGQTSHTTGGTGAADQFQWGYCFKEEISKATSPYYGRGPIQLTGRSNYDLA 141
DB 1 ELAAFFGQTSHTTGGTGRSSDQFQWGYCFKEEINKATSPYYGRGPIQLTGRSNYQRA 60

QY 142 RAIGKDLVSNPDVSTDAVVFRTAMFWMTAQGNKPSCHNVALRWTPTAATTAAGRVP 201
DB 61 NALGLDLVGNPDVSTDAVVFRTALWMTAQGNKPSCHDVILGWTFSAADTAAYRVP 120

QY 202 YGVITNIINGLEGCGMRDANVDRIGYTRYCYGMLGTATGNLDCYTORNFA 256
DB 121 GYDGLTNIINGLEGCGVGNANDVDRIGYTRYCYGMLGTATGNLDCYQNRNFA 175

RESULT 14
OB2552 PRELIMINARY; PRT; 253 AA.
AC 082552;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE CLASS II.
GN CHIAO OR CACH12.
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OC NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HANBYUL; TISSUE=LEAF;
RA Hwang B.K., Hong J.K., Kim Y.J.;
RT "Molecular cloning and characterization of a pathogen-induced gene
RT encoding a basic class II chitinase from Capsicum annuum.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091235; AAC36359.1; -.
DR HSP; P23951; 2BAA.
DR Mendel; 33139; Capan; Chiao; 33139.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
SQ SEQUENCE 253 AA; 27768 MW; F464515215B62251 CRC64;

Query Match 59.4%; Score 808.5; DB 10; Length 253;
Best Local Similarity 59.4%; Pred. No. 8.3e-62;
Matches 151; Conservative 32; Mismatches 64; Indels 7; Gaps 3;

QY 4 FALAVCAALLLAVAAGAAAGAGVSVITRSVYASMLPNDNSLCIPARGFTYDAFIAA 63
DB 3 FSVSPVALSCLFELFLITLITLQNTGSIYTRDLFERMLSRNNAACPGKGYTFEAFITA 62
QY 64 ANTFPGFGTGSADDIKRDLAFFGQTSHTTGGTGAADQFQWGYCFKEEISKATSPY 123

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QY 230 YTRYCGMLGTATGGLDCYTORNE 254
Db 240 FYKRYCDILKIGYGSNLDCAHQHF 264

Search completed: May 3, 2002, 18:46:59
Job time: 883 sec

Db 63 ANSFPAFGTGTGNTARKKVAFAFFGQTSSEINGRAGT---FNGGYCFVRQIDQ--SDRX 117
QY 124 YGRGPOLTGRSNYDLAAGRAI--GKDLVSNPDVLSTDAVVSFTAMFWMTAGNKPSCS 181
Db 118 YGRGPOLTGRSNYDLAAGRAI--GKDLVSNPDVLSTDAVVSFTAMFWMTAGNKPSCS 177
QY 182 NVALLRWTFATADTAAGRYPGYGVITNIINGGLECGMGRNDANDVDRIGYTRYCGMLSTA 241
Db 178 DVTIIGRWKSPADRSANRPVGYGVITNIINGGLECGMGRNGAVESRIGFYKRYCGMLNWP 237
QY 242 TGNLDCYTORNEFA 255
Db 238 TGNLDCYNQKNEFA 251

RESULT 15
042515
ID Q42515 PRELIMINARY; PRT; 264 AA.
AC Q42515;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHIA2 OR CHIA2,2.
OS Arachis hypogaea (Peanut).
OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; fabaceae; Papilionoideae; Arachis.
OX NCBI_TaxID=3818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NC 4;
RX MEDLINE=96178874; PubMed=8616259;
RA Kellmann J.W., Kleirow T., Engelhardt K., Philipp C., Wegener D.,
RA Schell J., Schreier P.H.;
RT "Characterization of two class II chitinase genes from peanut and
RT expression studies in transgenic tobacco plants.";
RL Plant Mol. Biol. 30:351-358(1996).
CC -/- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X82330; CAA57774.1; -.
DR HSSP; P23951; 2BAA.
DR Mendel; 1624; Arachis; Chia2; 1624.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
KW Hydrolase; Glycosidase.
SQ SEQUENCE 264 AA; 28924 MW; CCB13C590ADB5D8A CRC64;

Query Match 59.1%; Score 805.5; DB 10; Length 264;
Best Local Similarity 57.4%; Pred. No. 1.6e-61;
Matches 152; Conservative 35; Mismatches 63; Indels 15; Gaps 4;

QY 3 RFAALAVCAALALLAVAGAAAGVSVTRSVYASMLPNRDNLSLCPARGFTIYDAFIA 62
Db 2 KFCNFFFTLALIVLQALGASADDAAGTITITPLYNELKHLTDSRCEAHGFYTYNAFVT 61
QY 63 AANTFPGFTIGSADDI--KEDLAFTGQISHETTTGGTGRGAADOFOWGYCF-----KBEI 115
Db 62 AARAPAPAFGTG--DDVTRKRELAAFGQTSHTTGGTGTNAPDEFENGWYCYLREQTKQEH 119
QY 116 SKATSP-----YGRGPILTGRSNYDLAAGRAIGKDLVSNPDVLSTDAVVSFTAMWF 169
Db 120 CDSQAPCPAGKQYGRGPILTSTNSNYLAGQAIAKADLNNPDVAVDAVISEKTAIWF 179
QY 170 WMTAGNKPSCHNVALRWTFATADTAAGRYPGYGVITNIINGGLECGMGRNDANDVDRIG 229
Db 180 WMTPOGNKPSCHDVTINAWRPTATDSAGRAPGYGVITNIINGGLECGMGRNTNSNRIG 239

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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:30:29 ; Search time 117.39 Seconds
(without alignments)
203.814 Million cell updates/sec

Title: US-09-534-229C-2

Perfect score: 1792

Sequence: 1 MSTLRACATAVLAVLAAA.....YGNLDCYNQLSPNVGLAAQ 323

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.ll101.*
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1792	100.0	323	22 AAB11488	Wheat chitinase pr
2	1294.5	72.2	319	22 AAB11489	Wheat chitinase pr
3	1290	72.0	318	20 AAW98079	Rye chitinase-like
4	1265	70.6	298	20 AAW98080	Rye chitinase-like
5	1230	68.6	336	13 AAR29019	RCHI0 chitinase pr
6	1230	68.6	336	16 AAR67969	Rice chitinase. o
7	1230	68.6	336	22 AAB67444	Amino acid sequenc
8	1177.5	65.7	324	12 AAB13275	Tobacco intracellu
9	1177.5	65.7	324	18 AAW31297	Nicotiana sp. intr
10	1177.5	65.7	324	21 AAB07513	Amino acid sequenc
11	1170	65.3	329	12 AAB15841	Basic chitinase 48

12	1163.5	64.9	292	18 AAW24554	Chitinase. Cucurb
13	1161	64.8	331	12 AAB11305	Chitinase encoded
14	1160	64.7	317	17 AAW00186	American elm chiti
15	1142.5	63.8	328	13 AAR20822	Sequence of endoch
16	1141.5	63.7	329	15 AAR56860	Endochitinase prec
17	1081.5	60.4	303	13 AAR20820	Sequence of a 302
18	1055	58.9	266	15 AAR52577	Chitinase G. Hord
19	1052.5	58.7	328	19 AAW64776	Floral organ-speci
20	930	51.9	2466	20 AAY05844	Banana ripening fr
21	879	49.1	243	20 AAW90169	C. ensiformis chit
22	827	46.1	259	21 AAB18902	A maize chitinase
23	818.5	45.7	254	12 AAB13274	Petunia extracellu
24	818.5	45.7	254	18 AAW31296	Petunia hybrida ex
25	818.5	45.7	254	21 AAB07512	Amino acid sequenc
26	809	45.1	253	16 AAR76714	Tobacco endochitin
27	798	44.5	256	22 AAB11487	Wheat chitinase pr
28	795	44.4	439	13 AAR28150	Sugar beet chitina
29	790	44.1	252	20 AAW98081	Rye chitinase-like
30	786	43.9	230	20 AAW98082	Rye chitinase-like
31	779.5	43.5	250	16 AAR76713	Wild tomato endoch
32	779.5	43.5	252	21 AAB18903	A maize chitinase
33	775.5	43.3	253	16 AAR76712	Wild tomato endoch
34	774	43.2	284	21 AAB18905	A maize chitinase
35	770.5	43.0	272	21 AAG28415	Arabidopsis thalia
36	770.5	43.0	280	21 AAG28414	Arabidopsis thalia
37	707.5	39.5	372	22 AAB28788	Protein encoded by
38	644.5	36.0	155	21 AAB18906	Amino acid sequenc
39	633	35.3	271	21 AAB18904	Amino acid sequenc
40	633	35.3	271	21 AAB18936	Sugar beet chitina
41	597.5	33.3	268	13 AAR28147	A maize chitinase
42	595.5	33.2	281	21 AAB18894	Sugar beet chitina
43	584	32.6	264	13 AAR28145	Sugar beet chitina
44	492	27.5	813	21 AAG53657	Arabidopsis thalia
45	480.5	26.8	328	21 AAB18899	A maize chitinase

ALIGNMENTS

RESULT 1
AAB11488
ID AAB11488 standard; protein; 323 AA.
AC AAB11488;
XX
DT 02-MAR-2001 (first entry)
XX Wheat chitinase protein homologous to rye chitinase.
DE
XX Wheat; chitinase; low temperature expression; hardened; plant;
KW snow mould resistance; psychophilic plant pathogen; rye.
OS Triticum aestivum.
XX
XX JP2000270866-A.
XX 03-OCT-2000.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX (HOKK-) HOKKAIDO NAGOY SHIKENBACHO.
XX WPI; 2001-027417/04.
XX
PT New low temperature expression chitinase gene for producing a plant
grade highly resistant to psychophilic plant pathogenic microbes
XX
PS Claim 4; Fig 2; 11pp; Japanese.
XX This invention describes novel wheat chitinase genes. The invention also
CC describes a method for the isolation of a low temperature expression

CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat PIL73438 (of high snow mould resistance). The genes are
 CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.
 XX
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1792; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2.6e-144;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTLRARCATAVLAVLAAAVPATAEQCGSQAGGAKCADCCLCCSOFGCGTTSDYCGP 60
 Db 1 mstlrarcatavlavlaaavpataeqcgsgaggaakadclccsfgcgttsdygcp 60
 QY 61 RCQSQCCTGCGGGGASIVSRDLFERFLHRNDACLARGFYTYDAFLAAGAFPAFGT 120
 Db 61 rcqsqctgcggggvasivsrdlferflhrndaaclargfytydaflaagaafpafgt 120
 QY 121 TGDLDTRKREVAAFGQTSHTTGGWTPADPGTFSWGYCFKQEGSPSYCDQADWPCA 180
 Db 121 tgdldtrkrevaafgqtshtttgwtapdpgtfswgycfkgqegspsycdqadwpc 180
 QY 181 PGKQYGRGPQLTHNYNYPAGRAIGVDLLNPNPDLVATDPTVAFKTAIWFWMTTQSNKP 240
 Db 181 pgkqygrgpiqlthnynyypagraigvdlldnnpdlvatdptvafktaiwfwmttqsnkp 240
 QY 241 SCHDVITGLWTPPTARDASAGRVPGYGVITNVINGIECGMGQNDKVADPRIGFYKRYCDIF 300
 Db 241 schdvtglwtpardasagrvpgygvitnvningiecmgqndkvadprigfyrkycdif 300
 QY 301 GIGYGNLDYCNQLSFNVGLAAQ 323
 Db 301 gigygnldcynqlsfnvglaaq 323

RESULT 2

AAB11489
 ID AAB11489 standard; protein; 319 AA.

XX AAB11489;

02-MAR-2001 (first entry)

Wheat chitinase protein homologous to spring wheat chitinase.

DE Wheat; chitinase; low temperature expression; hardened; plant;
 KW snow mould resistance; psychophilic plant pathogen; spring wheat.

XX Triticum aestivum.

XX JP2000270866-A.

XX 03-OCT-2000.

XX 25-MAR-1999; 99JP-0081694.

XX 25-MAR-1999; 99JP-0081694.

XX (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.

XX WPI; 2001-027417/04.

XX New low temperature expression chitinase gene for producing a plant
 PT grade highly resistant to psychophilic plant pathogenic microbes -

XX Claim 7; Fig 3; 11pp; Japanese.

XX This invention describes novel wheat chitinase genes. The invention also
 CC describes a method for the isolation of a low temperature expression
 CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat PIL73438 (of high snow mould resistance). The genes are

CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.
 XX
 SQ Sequence 319 AA;

Query Match 72.2%; Score 1294.5; DB 22; Length 319;
 Best Local Similarity 71.0%; Pred. No. 4.5e-102;
 Matches 223; Conservative 34; Mismatches 48; Indels 9; Gaps 1;
 QY 12 VLAVLAAAVTATATACQCSQAGGAKCADCCLCCSOFGCGTTSDYCGPRCQSQCTCGG 71
 Db 5 vvvamlaaafavsaahaeqcgsgaggaatcpnclccskfsgcgttsdygctgcqsgcgcsg 64
 QY 72 G-----GGGVASIVSRDLFERFLHRNDACLARGFYTYDAFLAAGAFPAFGT 122
 Db 65 gtpvptpsggvgssliisqslfdqmlhrndaaclargfytydaflaagaafsfatg 124
 QY 123 DLDRKREVAAFGQTSHTTGGWTPADPGTFSWGYCFKQEGSPSYCDQADWPCA 182
 Db 125 stdvkrrevaafgqtshtttgwtapdpgtfswgycfkgqegspsycdqadwpcap 184
 QY 183 KOYXGRGPQLTHNYNYPAGRAIGVDLLNPNPDLVATDPTVAFKTAIWFWMTTQSNKP 242
 Db 185 kkyfgrgpiqlthnynyypagraigvdlldnnpdlvatdptvafktaiwfwmtpskps 244
 QY 243 HDVITGLWTPPTARDASAGRVPGYGVITNVINGIECGMGQNDKVADPRIGFYKRYCDIFGI 302
 Db 245 hdvitgrwspsgadgaagrvpgygvitnvningiecmgqndkvadprigfyrkycdilgv 304
 QY 303 GYGNLDYCNQLSF 316
 Db 305 sygnldcynqrpf 318

RESULT 3

AAW98079
 ID AAW98079 standard; protein; 318 AA.

XX AAW98079;

21-JUN-1999 (first entry)

DE Rye chitinase-like protein CHT9 preprotein.

XX CHT9; chitinase-like protein; antifreeze protein; APP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.

XX Secale cereale.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein /note= "signal peptide"

FT Protein 21..318

XX /note= "mature protein, also claimed in Claim 10"

PN WO9906565-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

XX (ICEB-) ICE BIOTECH INC.

XX Griffith M, Hew C, Moffatt B, Xiong F;

XX WPI; 1999-153795/13.

XX N-PSDB; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -

PT particularly with chitinase activity, used to impart frost, and
PT pathogen, resistant to plants, for preservation of foods, cells etc.
XX and for treating tumours

XX Claim 10; Fig 21a; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CC CHN9 preprotein. The mature protein, which is also claimed, is a
CC chitinase-like protein that has chitinase (antifungal) and
CC antifreeze activities. CHN9 cDNA (see AAX24889) was obtained by
CC isolating mRNA from rye plants grown at low temperatures in the
CC absence of pathogens or other stresses, i.e. under conditions when
CC only chitinases with antifreeze activity would be expressed. CHN9
CC and CHN46 (see AAW98081-82) have been cloned and expressed in
CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
CC The chitinase-like antifreeze proteins can be used: to increase
CC freezing tolerance of plants and microorganisms; to increase field
CC survival of plants, animals and microorganisms exposed to sub-zero
CC temperatures; to inhibit ice recrystallisation in biological
CC materials or foods; for cryopreservation and hypothermic protection
CC of cells, embryos, tissues etc. (particularly human platelets); and
CC to kill tumour cells. They are also used to inhibit initiation and
CC progression of diseases or spoilage caused by low temperature
CC pathogens (particularly fungi) in plants, frozen foods and any
CC cryopreserved biological material. The signal peptide can be used
CC to direct protein secretion in transgenic organisms or expression
CC systems.

XX Sequence 318 AA;

Query Match 72.0%; Score 1290; DB 20; Length 318;
Best Local Similarity 71.2%; Pred. No. 1.1e-101;
Matches 223; Conservative 34; Mismatches 48; Indels 8; Gaps 1;

QY 12 VLAVLAAAVTPATAQCGAGGAKADCLCCSOFGCGTTSYCGPRCQSQCTGCGG 71

DB 5 VVVMALAAFAVSAHAEGCGSAGGATGATCPCNCLCCSKFSGTSEYCGDGCQGCNRCGG 64

QY 72 -----GGGGVASIVSRDLFRFLHNRDAACLAGFYTYDAFLAAGAFPAFGTGD 123

DB 65 TPVPVPTPTGGGVSSLSLFDQMLHNRDAACLAGFYTYDAFLAAGAFPAFGTGD 124

QY 124 LDPKREVAFFGCTSHETGWTAPDGFPSWGYCFKQBGSPSPSYCDQADWPCAPGX 183

DB 125 TVRKREVAFLAQTSHETGWTAPDGFPSWGYCFKQBGSPSPSYCDQADWPCAPGX 184

QY 184 QYXGRGPIQLTHNYNGPAGRAIGVDLLNPDIVATDPTVAFKTAIWFWMTOSNKPESCH 243

DB 185 KYFGPGPIQISYNYPAGRAIGTDLNPDIVATDPTVAFKTAIWFWMTOSNKPESCH 244

QY 244 DVTGTLWTPARDSAAGRVPGYGVITNVIINGTECGMGQNDKVADRIGFYKRYCDIFGIG 303

DB 245 DVATGRWSPGDAQGAQVRPGYGVITNVIINGTECGMGQNDKVADRIGFYKRYCDIFGIG 304

QY 304 YGNLDCYNOLSF 316

DB 305 YGNDLDCYNQRPF 317

RESULT 4

AAW98080

ID AAW98080 standard; Protein; 298 AA.

XX AAW98080;

XX 21-JUN-1999 (first entry)

XX Rye chitinase-like protein CHN9.

DE CHN9; chitinase-like protein; antifreeze protein; AFP;
KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW transgenic plant; preservation; cryopreservation; tumour; therapy.

XX Secale cereale.

XX WO9906565-A2.

PN 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

XX (ICEB-) ICE BIOTECH INC.

XX Griffith M, Hew C, Moffatt B, Xiong F;

XX WPI; 1999-153795/13.

XX N-PSDB; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -
PT particularly with chitinase activity, used to impart frost, and
PT pathogen, resistant to plants, for preservation of foods, cells etc.
PT and for treating tumours

XX Claim 10; Fig 21d; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CC CHN9 mature protein. It lacks the 20-amino acid signal peptide
CC of the preprotein (see AAW98079), which is also claimed. Mature CHN9
CC is a chitinase-like protein that has chitinase (antifungal) and
CC antifreeze activities. CHN9 preprotein cDNA (see AAX24889) was
CC obtained by isolating mRNA from rye plants grown at low temperatures
CC in the absence of pathogens or other stresses, i.e. under conditions
CC when only chitinases with antifreeze activity would be expressed.
CC CHN9 and CHN46 (see AAW98081-82) have been cloned and expressed in
CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
CC The chitinase-like antifreeze proteins can be used: to increase field
CC freezing tolerance of plants and microorganisms; to increase survival
CC of plants, animals and microorganisms exposed to sub-zero
CC temperatures; to inhibit ice recrystallisation in biological
CC materials or foods; for cryopreservation and hypothermic protection
CC of cells, embryos, tissues etc. (particularly human platelets); and
CC to kill tumour cells. They are also used to inhibit initiation and
CC progression of diseases or spoilage caused by low temperature
CC pathogens (particularly fungi) in plants, frozen foods and any
CC cryopreserved biological material.

XX Sequence 298 AA;

Query Match 70.6%; Score 1265; DB 20; Length 298;
Best Local Similarity 72.7%; Pred. No. 1.3e-99;
Matches 216; Conservative 32; Mismatches 41; Indels 8; Gaps 1;

QY 28 EOCGSOAGGAKADCLCCSOFGCGTTSYCGPRCQSQCTGCGG-----GGGGVASI 79

DB 1 EQCGSGAGGATCPCNCLCCSKFSGTSEYCGDGCQGCNRCGGTVPVPTPTGGGVSSI 60

QY 80 VSRDLFRFLHNRDAACLAGFYTYDAFLAAGAFPAFGTGDTPKREVAFFGQTS 139

DB 61 ISQSLFDQMLHNRDAACLAGFYTYDAFLAAGAFPAFGTGDTPKREVAFFGQTS 120

QY 140 HETGWTAPDGFPSWGYCFKQBGSPSPSYCDQADWPCAPGXQYXGRGPIQLTHNYN 199

DB 121 HETGWTAPDGFPSWGYCFKQBGSPSPSYCDQADWPCAPGXQYXGRGPIQLTHNYN 180

QY 200 GPAGRAIGVDLLNPDIVATDPTVAFKTAIWFWMTOSNKPESCHDVTGLTPTARD 259

DB 181 GPAGRAIGVDLLNPDIVATDPTVAFKTAIWFWMTOSNKPESCHDVTGLTPTARD 240

QY 260 GRVPGYGVITNVIINGTECGMGQNDKVADRIGFYKRYCDIFGIGYGNLDCYNOLSF 316

DB 241 GRVPGYGVITNVIINGTECGMGQNDKVADRIGFYKRYCDIFGIGYGNLDCYNOLSF 297

QY	175	ADWPCAPGKOYVGRGPOTLTHNNYNGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT	233
Db	178	aqwpcagkxygrgpiqlsynfnyppagalgadllgpdllvasdatvsfdtafwmt	237
QY	235	TQNKPSCHDVIITGLWPTTARDSAAGRVPGYGVTVITVINGIGICGMGQNDKVADRIGFYK	294
Db	238	pqspkscnavatqwtwpsaddgragrvpygvtitnlingglecghgeddriadrigrfky	297
QY	295	RYCDIFGIGYGNNLDCYNO 313	
Db	298	rycdilgvsyganldcysq 316	
RESULT	6		
AA067969			
ID	AA067969	standard; Protein; 336 AA.	
XX			
AC	AA067969;		
DT	13-AUG-1995	(first entry)	
XX			
DE	Rice chitinase.		
XX			
KW	Chitinase; transgenic plant; disease resistance;		
KW	crop improvement; tobacco; Nicotiana tabacum; plant defense;		
KW	fungus pathogen; Cercospora nicotinae;		
KW	Thanatephorus cucumeris.		
XX			
OS	Oryza sativa.		
XX			
PN	WO9502319-A.		
XX			
PD	26-JAN-1995.		
XX			
EF	15-JUL-1994; 94WO-US07815.		
XX			
PR	16-JUL-1993; 93US-0093372.		
XX			
FA	(SALK) SALK INST BIOLOGICAL STUDIES.		
XX			
PI	Dixon RA, Lamb CJ, Maher EA, Zhu Q;		
XX			
XX	WPI; 1995-067090/09.		
DR	N-ESDB; AA081346.		
XX			
PT	Transgenic plants contg. several plant defence associated		
PT	proteins - have increased resistance to plant pathogens when		
PT	grown in crops as a food source		
XX			
PS	Disclosure; Page 31-32; 45pp; English.		
XX			
CC	The SphI fragment of rice chitinase RCH10 gene (given in AA081346) and		
CC	an alpha beta-1,3-glucanase coding sequence (AA081347) were		
CC	incorporated into vectors for co-expression in transgenic tobacco,		
CC	resulting in improved resistance to Cercospora nicotinae and		
CC	Thanatephorus cucumeris fungal infection.		
XX			
SQ	Sequence 336 AA;		
Query Match	68.6%;	Score 1230; DB 16; Length 336;	
Best Local Similarity	69.3%;	Pred. No. 1.4e-96;	
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps			
QY	4	LRACATAVIAVLAAAVTPATACQSGQAGKACDLCOSQFGCTSDYCGPRCQ 63	
Db	1	mrallavmavrfjlaaay---haeqcgsqgagvcpncliccqlfwcgtsdycgagcqq 57	
QY	64	SOCT-----CGCGGGGGVASIVSRDLFERFLHRNDAACLARGFTTYDAFLAAAGAF 11	
Db	58	sgostlrrrrdasaqgsvasivsrslfdlllhrndaacpsqsfvtdafvaasaf 11	

QY 116 PAFGTGDLTRKREVAFFGQTSHTTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
 Db 118 pfaaagdadnkrrevaafagtshtttggwatapdgytwgycfkeengagapdyccqs 177
 QY 175 ADWPCAPGQYYGRGPIQLTHNYNGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWEMWT 234
 Db 178 aqwpcaagkkygrgpiqlsynfygpaqgaigadllgdpdlvasdatvstafwmt 237
 QY 235 TQSNKPSCHDVITGLWTTARDSAAGRVPGYGVINNVINGGIECGMGONDKVADRIGFYK 294
 Db 238 ppspkpsnavatgwtspadddragrvpvygvitnllnggiecggeddriadrigfyk 297
 QY 295 RYCDIFGIGYGNLDCYNQ 313
 Db 298 rycdilgvsyganldcysq 316

RESULT 7
 AAB67444
 ID AAB67444 standard; Protein; 336 AA.
 XX AAB67444;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Amino acid sequence of a rice chitinase designated RCH10.
 XX
 KW Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase;
 KW Xanthomonas; plant pathogen; Brill protein; RCH10 protein.
 XX
 OS Oryza sp.
 XX
 PN WO200109283-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-US20714.
 XX
 PR 28-JUL-1999; 99US-0363313.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Ronald P, He Z, Chory J, Lamb C, Li J;
 XX
 DR WPI; 2001-159858/16.
 DR N-PSDB; AAF54983.

XX Chimeric plant receptors comprising a polynucleotide encoding a RPK
 PT receptor containing a heterologous extracellular domain and a kinase
 PT domain from a Xa21 polypeptide, useful for modulating plant responses
 PT to pathogens
 XX
 PS Disclosure; Page 45-46; 47pp; English.
 XX
 CC The present sequence represents a chitinase designated RCH10. The
 CC specification describes chimeric receptors which are used for modulating
 CC plant responses to pathogens. The receptors comprise a heterologous
 CC extracellular domain (e.g. from a Brill protein or RCH10 protein) and
 CC a kinase domain (e.g. from disease resistance protein Xa21). The Xa21
 CC gene is a member of disease resistance genes referred to as RKK genes.
 CC When Xa21 is present in a transgenic plant, it confers resistance to
 CC Xanthomonas spp.. The plant receptors containing heterologous domains
 CC are useful for modulating plant responses to pathogens including viruses,
 CC bacteria, nematodes, fungi or insects. The nucleic acids can be used to
 CC confer desired traits on essentially any plant.
 XX
 SQ Sequence 336 AA;

Query Match 68.6%; Score 1230; DB 22; Length 336;
 Best Local Similarity 69.3%; Pred. No. 1.4e-96;
 Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

QY 4 LRARCATAVLAVLWIAAAAVTPATABEQCSQAGGAKACDCLCCSQBFGCGTTSDDYCGPRCQ 63
 Db 1 mralavvamvarpfilaav---haeqcgsgagavcpncloesqfgwsgstsdycgagcq 57
 QY 64 SQCT-----GCGGGGGVASIVSRDLFEFLHNRDAACLARGFVTDYDAFLAAAGAF 115
 Db 58 sqcsrlrrrrpdasggsgvasivsrslfdlmlhndaacpasnftydafvaasaf 117
 QY 116 PAFGTGDLTRKREVAFFGQTSHTTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
 Db 118 pfaaagdadnkrrevaafagtshtttggwatapdgytwgycfkeengagapdyccqs 177
 QY 175 ADWPCAPGQYYGRGPIQLTHNYNGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWEMWT 234
 Db 178 aqwpcaagkkygrgpiqlsynfygpaqgaigadllgdpdlvasdatvstafwmt 237
 QY 235 TQSNKPSCHDVITGLWTTARDSAAGRVPGYGVINNVINGGIECGMGONDKVADRIGFYK 294
 Db 238 ppspkpsnavatgwtspadddragrvpvygvitnllnggiecggeddriadrigfyk 297
 QY 295 RYCDIFGIGYGNLDCYNQ 313
 Db 298 rycdilgvsyganldcysq 316

RESULT 8
 AAR13275
 ID AAR13275 standard; Protein; 324 AA.
 XX AAR13275;
 XX
 DT 14-OCT-1991 (first entry)
 XX
 DE Tobacco intracellular chitinase.
 XX
 KW fungal resistance; phytopathogen.
 XX
 OS Nicotiana tabacum Samsun NN.
 XX
 EH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal peptide
 FT 24..324
 FT /label= intracellular chitinase
 XX
 PN EP440304-A.
 XX
 PD 07-AUG-1991.
 XX
 PF 30-JAN-1991; 91EP-0200191.
 XX
 PR 30-JAN-1990; 90NL-0000222.
 XX
 PA (MOGE-) MOGEN INT NV.
 PA (UYLE-) RIJCSUNIV TE LEIDEN.
 XX
 PI Cornelissen BJ, Melchers LS, Meulenhoff EJ, Van Roekel JS;
 PI Sela-Buurlage MB, Vloemans AA, Woloshuk CP, Bol JF;
 XX
 DR WPI; 1991-232019/32.
 DR N-PSDB; AAQ12898.
 XX
 PT Plants with improved resistance to pathogenic fungi - contains
 PT chitinase and/or beta-1,3-glucanase genes modified for
 PT over-expression targeted to apoplasts
 XX
 PS Example 4; Fig 2; 55pp; English.
 XX

CC The sequence from which this amino acid was deduced was isolated
 CC from a N.tabacum cDNA library following screening with a partial
 CC tobacco intracellular chitinase clone. The protein sequence appears
 CC twice in the specification but in one (not the one given in this

CC file), the Leu codons at positions -23, -21, -15, -12, -11, -8, -7,
CC -5, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266,
CC 274, 286 are translated as Ile.
CC See AAC12897-012900.

XX	Sequence	324 AA;
S0		

Query Match	65.7%	Score 117.5;	DB 12;	Length 324;
Best Local Similarity	64.2%	Pred. NO. 3.9e-92;		
Matches 203;	Conservative	45;	Mismatches 65;	Indels 3;
				Gaps 2;

[illegible]

QY 125 DTRKREVAFFGQTSHTETGGWPTADPGPESWGYCFKQEGSPPSYCDQSDADWPCAPQZ 184

185 YYGRGPIQLTHNYNYPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244

Db 184 yfgrgprqismnynygpcgralgvuulmpurvacupvzkrkcazmmefp-f-
245 VITGIWTPTDASAAGRVPBGYVITNVINGGIECMGQNDKVADRIGFKRYCDIFGICY 304

Db 244 vii gr w p s s a d r a a n l p g f v i t n i n g g l e c g r g t d s r v q d r i g f y r y c s a l g v s p 300

```
Db 304 gdnldcgngsfngl 319
```

RESULT 9
AAW31297

XX AC AAW31297;

DI 11-MAR-1956 (first entry)
 XX
 XX Nicotiana sp. intracellular chitinase protein.
 DE

KW Intracellular chitinase; antifungal; synergism;
KW beta-1,3-glucanase gene; tobacco.

OS	Nicotiana sp.	
XX		Location/Qualifiers
FX		

FT	Protein	/label= signal_peptide	24..324
FT	Protein	/label= signal_peptide	24..324

XX
PN
v
v
US5670706-A.

XX 19-APR-1993; 93US-0047413.

PR 29-JAN-1991; 91US-0647831.
XX
XX

XX	Linthorst HJM, Melchers LS;
PT	Cornelissen BJC,
PA	Bol JF.
{OYLE-} RIJKSONIV LEIDEN.	

PI Vloemans AA, Woloshuk CP;
XX

WPI; 1997-479536/44.
N-PSDB; AAT89952.

Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase

Example 4: Fig 2; 42pp; English.

This sequence represents an intracellular chitinase which is used to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait, plants that overexpress the chitinase and glucanase genes exhibit a synergistic antifungal effect.

Sequence 324 AA;

Query Match	65.7%;	Score 1177.5;	DB 18;	Length 324;
Best Local Similarity	64.2%;	Pred. No. 3.9e-92;		
Matches 203:	Conservative	45;	Mismatches 65;	Indels 3;
				Gaps 2;

Qy 8 CATAVLAVLAAAAVTPATAEQCSQAGGAKCADCICCSQFGCTTSDYICP-RCQSQC 66

D6 4 cktalsslllililsasaeqgsqaygarcsagfcccckrgagsgg-
67 TG--CGGGGGGVAStVSRLFERELLHRNDACIARGFYTYDAFLAAGAFPAFGTTGDL 124

Db 64 pggtpppggd_lgsliissmfdqmlxhnrndnaoqgkgyfsynafinaaarsifbgrtsguc 184

Db 124 tarkrelaaffagtsbettggwatpdgpyawgycwltregecspgdyctpsggwpocapgrk 183

QY 163 i i g r o f i q i h n y n y p g c g r a i g v d l n n p d l v a t d p v i s f k s a l w f w m t p q s k p s c h d 243

pb 184 v f a r g i q i s h n y n y p g c g r a i g v d l n n p d l v a t d p v i s f k s a l w f w m t p q s k p s c h d 243

QY 245 VITGLWPTARSDAAGRVPVGVITNVINGGLECGNQNDRAVDRIQFIRAKICQI 303

0V 305 GNNLDCYNQLSFENVGL 320

Db 304 gdnldcgnqrsfgngl 319

RESULT 10
AAB07513
IS AAB07513 standard: Protein: 324 AA.

AA
AC AAB07513;

XX
RE
20-00m-2000 (first entry)-XX Leucocytin leucocytinase

XX Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;
KW Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;
KW Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;
KW Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;

XX Nicotiana sp.

XX	Key	Location/Qualifiers
FH		
FT	Peptide	1..23

XX
DN
US6087560-A

XX

FD XX

```

PF 18-FEB-1997; 97US-0801563.
XX
XX 19-APR-1993; 93US-0047413.
PR 29-JAN-1991; 91US-0647831.
XX
XX (OYLE-) RIJKSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
XX
XX Cornelissen BJC, Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
PI Vloemans AA, Woloshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
XX
XX WPI: 2000-498214/44.
DR N-PSDB; AAA58910.
XX
XX New transgenic plants expressing chitinase and glucanase have improved
PT resistance against pathogenic fungi, particularly against Alternaria
PT alternata or Fusarium oxysporum f. sp. lycopersici -
XX
XX Example 4; Fig 2A-B; 42pp; English.
PS
XX The present sequence represents an extracellular chitinase. The
CC specification describes transgenic plants which express a chitinase
CC gene and a glucanase gene. The expression of the chitinase and
CC beta-1,3-glucanase genes produces an antifungal effect. The transgenic
CC plants are useful for improving plant resistance to pathogenic fungi.
CC The recombinant polynucleotides and the process are useful for
CC producing fungal resistant plants.
XX
XX Sequence 324 AA;
SQ
Query Match 65.7%; Score 1177.5; DB 21; Length 324;
Best Local Similarity 64.2%; Pred. No. 3.9e-92;
Matches 203; Conservative 45; Mismatches 65; Indels 3; Gaps 2;
QY 8 CATAVLAVLVAAAATPATAEQCSQAGGAKACDCLCCSQFGCGTTSYCGP-RCQSQC 66
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 ckftalsllfslillsaeeqcsqaggarccsglccskfsgcgtntndycgpnwqsc 63
QY 67 TG--CGGGGGVASIVSRDLFERFLHRNDAACLARGFYTDFAAAGAFPAFGTTGDL 124
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 ppgtpppggdslsllssmfdgmklhrndnacqgkfysynafinaarsfpfgtsagt 123
QY 125 DTRKREVAAPFGQTSHETTGWPTAPDPGFSWGYCFKQEGSPSYCDQADWPCAPGKQ 184
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 tarkreiaafagtshtetggwatapdgyawycwlrqcspgdyctpsgqwpcabgrk 183
QY 185 YGRGPIQLTHNNYGPAGRAIGVDLLNPNLVATDPTVAEKTALWMTQSNKPSCHD 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 yfgrgpiqishnynygcgraignvdlldnnpdlvatdpsvisksalwfmtpqspkpschd 243
QY 245 VITGLWPTARDAAGRPVGYVTINVGIECGMGQNDKVDADRIGFYKRYCDIFGIGY 304
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 vilgrwpsadraanrlpfgvltningglecgrgtdsrqgrigfyrriycsilgvsp 303
QY 305 GNNLDCYNQLSFNVGL 320
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 gdnldcgnqrsfngl 319
RESULT 11
ID AAR15841
XX AAR15841 standard; Protein: 329 AA.
XX
XX AAR15841;
AC AAR15841;
XX
XX 19-MAR-1992 (first entry)
DT
XX Basic chitinase 48 from clone lambdaCHN17.
XX
XX Vacuole; targeting; chitinase; glucanase; signal; resistance;
KW pharmaceutical; hormones; expression; secretion; extracellular.
XX

```

```

OS Nicotiana tabacum L. C.V. Havana 425.
XX
XX Key Location/Qualifiers
FH 1..148
FT Region /label= exon1_prod.
FT 149..199
FT Region /label= exon2_prod.
FT 200..329
FT Region /label= exon3_prod.
FT 318..329
FT Peptide /label= sig_peptide
FT /note= "used as vacuole targeting peptide"
XX
XX EP462065-A.
PN
XX 18-DEC-1991.
PD
XX 06-JUN-1991; 91EP-0810430.
PF
XX 15-JUN-1990; 90CH-0002007.
PR
XX (CIBA ) CIBA GEIGY AG.
PA
XX Bollier T, Nauhaus JM, Ryals J;
PI
XX WPI: 1991-371028/51.
DR N-PSDB; AAQ15147.
XX
XX DNA sequence encoding vacuole targeting peptide - esp. signal
PT region of tobacco chitinase or glucanase gene, and derived
PT recombinant DNA, vectors, etc. functional in plants
XX
XX Disclosure; Page 64-68; 81pp; English.
PS
XX Attachment of the signal peptide ensures occlusion of expressed
CC prod. in the vacuole while elimination of the signal peptide from
CC a sequence normally contg. it ensures that the expressed product
CC is secreted into the extracellular space, rather than retained in
CC the vacuole. Recombinant DNA may contain a structural gene which
CC protects the plant, e.g. resistance to pathogens, herbicides,
CC insecticides, biocides, environmental stress, etc.; leads to
CC increased prodn. of proteins, carbohydrates, etc.; or encodes for
CC pharmaceuticals such as hormones or immunomodulators.
CC See also AAQ15146-50 and AAQ15330-35.
XX
XX Sequence 329 AA;
SQ
Query Match 65.3%; Score 1170; DB 12; Length 329;
Best Local Similarity 63.2%; Pred. No. 1.7e-91;
Matches 203; Conservative 44; Mismatches 66; Indels 8; Gaps 2;
QY 8 CATAVLAVLVAAAATPATAEQCSQAGGAKACDCLCCSQFGCGTTSYCGP-RCQSQC 66
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 ckftalsllfslillsaeeqcsqaggarccsglccskfsgcgtntndycgpnwqsc 63
QY 67 TG-----CGGGGGVASIVSRDLFERFLHRNDAACLARGFYTDFAAAGAFPAFG 119
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 ppgtppptpppggdslsllssmfdgmklhrndnacqgkfysynafinaarsfpfg 123
QY 120 TTGDLDTKREVAAPFGQTSHETTGWPTAPDPGFSWGYCFKQEGSPSYCDQADWPC 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 tsqdtarkreiaafagtshtetggwatapdgyawycwlrqcspgdyctpsgqwp 183
QY 180 AFGKQYGRGPIQLTHNNYGPAGRAIGVDLLNPNLVATDPTVAEKTALWMTQSNK 239
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 apgrkyfgrgpiqishnynygcgraignvdlldnnpdlvatdpsvisksalwfmtpqspk 243
QY 240 PSCHDVITGLWPTARDAAGRPVGYVTINVGIECGMGQNDKVDADRIGFYKRYCDI 299
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 pschdvilgrwpsadraanrlpfgvltningglecgrgtdsrqgrigfyrriycsi 303
QY 300 FGIGYGNLDCYNQLSFNVGL 320

```

```

Db 304 lgvspgdnldcgnqrsfngl 324
      | : ||||| || || ||
RESULT 12
AAW24554
ID AAW24554 standard; Protein; 292 AA.
XX
AC AAW24554;
XX
XX 10-OCT-1997 (first entry)
XX DT
XX DE
XX DE
XX KW Chitinase;
XX KW Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase;
XX KW fungal cell membrane; pathogenic fungus; disease resistance; chitin.
XX OS
XX OS Cucurbita pepo.
XX PN
XX PN JP09163987-A.
XX PD
XX PD 24-JUN-1997.
XX PF
XX PF 14-DEC-1995; 95JP-0347367.
XX PR
XX PR 14-DEC-1995; 95JP-0347367.
XX PA (NIHA ) JAPAN ENERGY CORP.
XX PA (SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
XX DR
XX DR WPI; 1997-380170/35.
XX DR N-PSDB; AAT79940, AAT79941.
XX PT
XX PT Chitinase derived from pumpkin - used to protect plants against
XX PT pathogenic fungi
XX PS
XX PS Claim 1; Page 2; 36pp; Japanese.
XX CC
XX CC This sequence represents the pumpkin chitinase. Chitinase is an enzyme
XX CC decomposing chitin (not present in plant cell membranes) found in the
XX CC cell membranes of fungi. Plants have this enzyme to protect themselves
XX CC from pathogenic fungi. Thus this enzyme can be used to prevent plants
XX CC from being infected with pathogenic fungi, and the chitinase gene can be
XX CC introduced into plants to improve their resistance to diseases caused by
XX CC fungi. As the amino acid sequence of the chitinase does not have any
XX CC region to be cleaved by ubiquitous peptidases in cells, the chitinase
XX CC produced by genetic recombination technology works for various host cells
XX CC and serves for plant immunity to confer disease resistance on plants as
XX CC the host.
XX SQ
XX SQ Sequence 292 AA;

Query Match 64.9%; Score 1163.5; DB 18; Length 292;
Best Local Similarity 69.6%; Pred. No. 5.3e-91;
Matches 204; Conservative 30; Mismatches 34; Indels 5; Gaps 2;

Qy 28 EQCGSQAGAKCADCCLCCSQFGCGTTSYDYGPRCQSQOC---TCGGGGGGGVASIVSRD 83
      ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| : |||||
Db 1 eqcrgangalcpnrlccsqfqcwqntdeycknccsqcqtppstggggggsvgsiinea 60
      | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Qy 84 LFERFLHRNDAAACIARGFYTYDAFLAAGAPFAPGTTGDLDTRRKREVAAPFGQTSHETT 143
      | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 61 lymqlkyskdpqpsngfryynafitaqsfsgfttgdaatrrelaafgqtsnett 120
      ||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Qy 144 GSWPAPDPFSWVCYFKQEQSPSYCQSDADWPCAPKQVYGRGPIQLTHNYNGPAG 203
      ||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 121 ggwaapdpayawgycfirer-nqdvycspnqgwpcaaqkkygr-gpiqlthnyngpag 179
      || : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Qy 204 RAIGVDLLNNPDLVATDPTVAFKTAIFWMTTCSNKPSCDHVITGLWPTARDASAAGRVP 263
      || : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 180 ralninllnppdlvatdpvvaftaiwmtpggnkpschdvtgrwpsaadsaagrwp 239
      || : : : : | : : : : | : : : : | : : : : | : : : : | : : : :

Qy 264 GYGVITNVINGGIECGMGQNDKVDADRIGFYKRYCYGIGNLDCYNQLSF 316
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 240 ggyvitnilinglecgrgadsrvadrigfykrycdlligyggnldcnnqrsf 292
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 13
AAR11305
ID AAR11305 standard; Protein; 331 AA.
XX
XX AAR11305;
XX
XX 30-MAY-1991 (first entry)
XX DT
XX DE
XX DE Chitinase encoded by genomic clone lambda CHN17.
XX KW Plant chitinase; transgenic plants; pathogen resistance.
XX KW Plant chitinase; transgenic plants; pathogen resistance.
XX OS
XX OS Nicotiana tabacum.
XX PN
XX PN EP418695-A.
XX PD
XX PD 27-MAR-1991.
XX PF
XX PF 10-SEP-1990; 90EP-0117389.
XX PR
XX PR 13-SEP-1989; 89CH-0003334.
XX PA (CIBA ) CIBA GEIGY AG.
XX PA
XX PA Meins F, Shinshi H, Neuhaus J-M;
XX PI
XX PI WPI; 1991-088356/13.
XX DR
XX DR N-PSDB; AAQ11093.
XX PT
XX PT New DNA regulatory sequence from new tobacco chitinase gene -
XX PT used to increase expression of foreign genes in transgenic
XX PT plants, partic for improving resistance to pathogens etc.
XX PS
XX PS Disclosure: page 44; 65pp; German.
XX CC
XX CC This recombinant tobacco chitinase gene prod. is encoded by a
XX CC genomic clone, lambda CHN17 which comprises 3 exons and has
XX CC 5'- and 3'- untranslated regions. A fragment (claimed) from
XX CC the 5'-untranslated region can be used to increase the ex-
XX CC pression of foreign genes in transgenic plants. The fragment
XX CC is linked to a foreign gene, eg chitinase or glucanase gene
XX CC via a spacer and is also linked to regulatory sequences. The
XX CC resultant DNA construct is used to transform plant cells, eg
XX CC tomato or tobacco, which subsequently produce the gene prod.
XX CC at a high level.
XX CC See also AAQ11094.
XX SQ
XX SQ Sequence 331 AA;

Query Match 64.8%; Score 1161; DB 12; Length 331;
Best Local Similarity 63.2%; Pred. No. 1e-90;
Matches 204; Conservative 44; Mismatches 65; Indels 10; Gaps 4;

Qy 8 CATAVLAVVLAATAATPATAEQCGSQAGAKCADCCLCCSQFGCGTTSYDYGPRCQSQOC 66
      | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 4 ckftalsllfslillsasaqcgsqaggarcpqslccskfqcwqntndygcpgncsqgc 63
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 67 TG-----CGGGGGGVASIVSRDLFERFLHRNDAAACIARGFYTYDAFLAAGAPFAG 119
      | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 64 psgppltaptppggdglgslsssmfdqmkhrnduacqgkfysynafinaarsfpqfg 123
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 120 ITGDLDTRRKREVAAPFGQTSHTTGGWTPADPGPFSWVCYFKQEQSPSYC-DQSDAPW 178
      | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 124 tsgdtarkrelaafactshettgwtatdpdyawgycwrlregspdyctpsgqwp 183
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 179 CAPG-KQYVGRGPIQLTHNYNGPAGRAIGVDLLNNPDLVATDPTVAFKTAIFWMTTQS 237
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

```

The inventors claim a new recombinant gene which codes for a protein with an endochitinase activity, or its precursor (see RAQ21007). The coding part of the gene contains at least the 5' part of DNA for tomato endochitinase and at least the 3' part of DNA for the tobacco enzyme (DNA can be genomic or cDNA, but at least one intron is preferred). The recombinant gene includes the 35S promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of *Agrobacterium tumefaciens*.

This sequence is encoded by the cDNA clone pH52, and represents a protein having chitinase-activity derived from american elm. This protein inhibits the fungus *Ophiostoma ulmi*, the causative agent of Dutch elm disease. The clone pH52 may be used to transform *E. coli* cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of elm trees.

Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 37, Appli
Sequence 35, Appli
Sequence 36, Appli
Sequence 10, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 8, Appli
Patent No. 5187262
Sequence 14, Appli

28 818.5 45.7 254 1 US-08-047-413-9
29 818.5 45.7 254 3 US-08-229-050-9
30 818.5 45.7 254 3 US-08-801-563-9
31 809 45.1 253 1 US-08-162-475A-5
32 784 43.8 253 4 US-07-791-931-9
33 781.5 43.6 253 1 US-08-162-475A-2
34 779.5 43.5 250 1 US-08-162-475A-4
35 765 42.7 316 4 US-07-791-931-8
36 707.5 39.5 372 4 US-07-791-931-4
37 512 28.6 130 3 US-08-329-799-37
38 437 24.4 148 3 US-08-329-799-35
39 232 12.9 51 3 US-08-329-799-36
40 213 11.9 211 2 US-08-935-886-10
41 212 11.8 71 1 US-07-704-288C-15
42 212 11.8 71 1 US-08-379-259-15
43 212 11.8 208 2 US-08-935-886-8
44 200.5 11.2 209 6 5187262-2
45 198 11.0 63 1 US-07-704-288C-14

ALIGNMENTS

RESULT 1
US-07-704-288C-3
; Sequence 3, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-704-288C-3

Query Match 68.6%; Score 1230; DB 1; Length 336;
Best Local Similarity 69.3%; Pred. No. 1 6e-103;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

5

QY 4 LRARCATAVLAVLVAAVPTAEQCGSQAGGAKADLCSCQFGCGTSDYCGPRCQ 63
DB 1 MRALAVVAVAREFLAAV---HAECGSGAGGAVCPNCLCCSQFGCGTSDYCGAGCQ 57

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:43:02 ; Search time 79.44 Seconds
(without alignments)
91.498 Million cell updates/sec

Title: US-09-534-229C-2
Perfect score: 1792
Sequence: 1 MSTLRARCATAVLAVLVAA.....YGNLDCYNQLSFNVGLAAQ 323

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1230	68.6	336	1 US-07-704-288C-3	Sequence 3, Appli
2	1230	68.6	336	1 US-08-093-372-2	Sequence 2, Appli
3	1230	68.6	336	1 US-08-379-259-3	Sequence 3, Appli
4	1177.5	65.7	324	1 US-08-047-413-11	Sequence 11, Appli
5	1177.5	65.7	324	3 US-08-229-050-11	Sequence 11, Appli
6	1177.5	65.7	324	3 US-08-801-563-11	Sequence 6, Appli
7	1176.5	65.7	310	4 US-07-791-931-6	Sequence 6, Appli
8	1167	65.1	310	1 US-07-704-288C-6	Sequence 6, Appli
9	1167	65.1	310	1 US-08-379-259-6	Sequence 6, Appli
10	1141.5	63.7	329	2 US-08-475-427-13	Sequence 13, Appli
11	1141.5	63.7	329	2 US-07-842-165-13	Sequence 7, Appli
12	1135.5	63.0	328	4 US-07-791-931-7	Sequence 9, Appli
13	1129	63.0	318	1 US-07-704-288C-9	Sequence 9, Appli
14	1129	63.0	318	1 US-08-379-259-9	Sequence 9, Appli
15	1126	62.8	328	4 US-07-791-931-5	Sequence 5, Appli
16	1120	62.5	330	1 US-07-704-288C-8	Sequence 8, Appli
17	1120	62.5	330	1 US-08-379-259-8	Sequence 8, Appli
18	1108.5	61.9	314	1 US-07-704-288C-7	Sequence 7, Appli
19	1108.5	61.9	314	1 US-08-379-259-7	Sequence 7, Appli
20	1077.5	60.1	302	2 US-08-475-427-6	Sequence 6, Appli
21	1077.5	60.1	302	2 US-07-842-165-6	Sequence 6, Appli
22	1055	58.9	266	4 US-08-812-025-10	Sequence 10, Appli
23	1055	58.9	266	4 US-07-791-931-10	Sequence 10, Appli
24	1055	58.9	266	4 US-09-138-873A-10	Sequence 10, Appli
25	986.5	55.1	254	2 US-08-475-427-1	Sequence 1, Appli
26	986.5	55.1	254	2 US-07-842-165-1	Sequence 1, Appli
27	986.5	55.1	254	4 US-08-448-398-3	Sequence 3, Appli

64	SOCT-----GCGGGGGV	ASIVSRDLFRFLHRNDAA	CLARGFTYDAFLAAGAF	115
58	SOCRLRRRRP	DASGGGGV	ASIVSRSLFDMLHRNDAA	CPASNFYDAFVAASAF
116	PAFGTTGDL	TRKREVA	AFQGTSHETTGMP	APDGFPSWGYCFKQSQ-GSPSYCQDS
118	PGFAAAGD	ADTNKREVA	FLAOTSHTTGGW	ATPDGFTWGYCFKEENGAGDPDYCOOS
175	ADWPCAPG	QKQYVGR	PIQLTHTNNTG	PAGRAICVDLLNNPDLVAIDPIVAKTALFWMT
178	ADWPCAG	KKQYVGR	PIQLSYNFNTG	PAGQAIGADLLGDPDLVSDATVSPDTAEFWMT
235	TGSNKP	SCHDVTGL	WTPATARDS	AGRVPFGVITVINVGTECGMGONDKVADFIGVK
238	POSPPK	SCNAVATG	WTFSDADQ	ARVPFGVITVINLGLECGHGEDDRADRIGYK
295	RYCDIF	FGIGYGN	LLDCYNQ	313
298	RYCDIL	GVSVG	ANLDCYSO	316

RESULT 2
 US-08-093-372-2
 ; Sequence 2, Application US/08093372
 ; Patent No. 5530187
 ; GENERAL INFORMATION:
 ; APPLICANT: Lamb, Christopher J.
 ; APPLICANT: Zhu, Qun
 ; APPLICANT: Maher, Eileen A.
 ; APPLICANT: Dixon, Richard A.
 ; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE
 ; TITLE OF INVENTION: DISEASE RESISTANCE GENES
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2921
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/093,372
 ; FILING DATE: 16-JUL-1993
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9391
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 336 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-093-372-2

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Query Match          68.6%;   Score 1230;   DB 1;   Length 336;
Best Local Similarity 69.3%;   Pred. No. 1.6e-103;
Matches 221;   Conservative 31;   Mismatches 15;   Indels 12;   Gaps 3;

4 LRARCATAVLAVLVAAAAVPTAAEQGGGAGAGAKADCLCCSQFGCTTSDYCGPPCQ 63
      :::::|||||
1 MEATAVVAVVAVRPPTAAV---HAEQGSAGAGVAPNCLCCSQFGCWGSTDYCGAGCQ 57

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& ~~de la~~
allanya

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-047-413-11

Query Match          65.7%; Score 1177.5; DB 1;
Best Local Similarity 64.2%; Pred. No. 8.4e-99;
Matches 203; Conservative 45; Mismatches 65;

QY      8 CATAVLVVLAANAATPATACQCSQAGGAKCADCILCCSFGRC
      | | | | | | | | | | | | | | | | | | | | | |
Db      4 CKFTALSSLLFELLILLSASAEQCSQAGGAFCAAGLCCSKPFW
      | | | | | | | | | | | | | | | | | | | | | |

QY     67 TG-CGGGGGGVASIVSRDLFERLLHRNDAAACIARGFYTYDAFLAAAGAFPAFGTGL 124
      | | | | | | | | | | | | | | | | | | | | | |
Db     64 PGGFTPPGGDGLGSISSMFDQMLKHNDCQKGKGYSYNAFNAARSFPGFGTSGDT 123
      | | | | | | | | | | | | | | | | | | | | | |

QY    125 DTRKREVAFFQCTSHETTGMPAPDGPFGSWGCFKQEQSPSICDQADWPAPGKQ 184
      | | | | | | | | | | | | | | | | | | | | | |
Db    124 TARKREIAFAAQTSHETTGWTAPDGPYAWGYCWLREQCSPGDCYCTPSGQWPCAPGRK 183
      | | | | | | | | | | | | | | | | | | | | | |

QY    185 YGREGPIQLTHNYNYPAGRAGVGLLNPNLVDTPVAFKTAIWFWMTQGNKPSCHD 244
      | | | | | | | | | | | | | | | | | | | | | |
Db    184 YFGREGPIQLSHNNYGPCGRAGVGLLNPNLVDTPVIFSKSALFWMTQSPKPSCHD 243
      | | | | | | | | | | | | | | | | | | | | | |

QY    245 VTGLWMTPTARSAAGRVPGYGVITNVINGGIECGMGQNDKVDRIQFYKRYCDIFIGY 304
      | | | | | | | | | | | | | | | | | | | | | |
Db    244 VIIGRWQPSADRAANELPFGVITNIINGLEGCRGTDTSRVQDRIGFYRKYCSILGVSP 303
      | | | | | | | | | | | | | | | | | | | | | |

QY    305 GNNLDCYNQLSFNVGL 320
      | | | | | | | | | | | | | | | | | | | | | |
Db    304 GDNLLDCGNQSRFNGVL 319
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5
US-08-229-050-11
; Sequence 11, Application US/08229050
; Patent NO. 6066491
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-229-050-11

Query Match 65.7%; Score 1177.5; DB 3; Length 324;
Best Local Similarity 64.2%; Pred. No. 8.4e-99;
Matches 203; Conservative 45; Mismatches 65; Indels 3; Gaps 2;

QY 8 CATAVLAVLAAAVTATACQCGSAGGACADCLCCSQFGCGTTSYDYGCP-RCQSQ 66
Db 4 CKFTALSSLLSLLSASAECQCGSAGGACASGLCCSKFGWCGNTNDYCGPNCQSQ 63
QY 67 TG--CGGGGGGVASIVSRDLFERLLHRNDAACLARGFYTYDAFLAAGAPPAGFTGDL 124
Db 64 PGGTPPGGGDLGSISSMFDQMLKHNDAACQKGFYSYNAFTNAARSPFGTSGDT 123
QY 125 DTRKREVAFFQGTSHETTGWPAPDGPFSWGYCFKQCGSPSYCDQSDADWPCAPGKQ 184
Db 124 TARKEIAAFAQTSHETTGWATAPDGPYAWGYCWLREQCSPGDCYCPGOWPCAPGRK 183
QY 185 YGRGPIQLTHNYGPGRAIGVDLLNPNLDVADPTVAEKTALWFWMTTQSNKPSCHD 244
Db 184 YFGRGPIQISHNYGPGRAIGVDLLNPNLDVADPTVISFKSALWFWMTTQSNKPSCHD 243
QY 245 VITGLWTPATDASAGRPVGYVTINWINGIECGMGQNDKVADRIGFYKRYCDIFGIGY 304
Db 244 VIIGRWQPSADRAANRLPGFVITNIINGGLECGRGTDTSRVQDRIGFYKRYCISILGVSP 303
QY 305 GNNLDCYNQLSFNVGL 320
Db 304 GDNLDGNGQSRFNGNL 319

RESULT 7
US-07-791-931-6
; Sequence 6, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikbel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

```

US-07-791-931-6

Query Match 65.7%; Score 1176.5; DB 4; Length 310;
Best Local Similarity 67.2%; Pred. No. 9.8e-99;
Matches 201; Conservative 41; Mismatches 54; Indels 3; Gaps 2;

QY 25 ATAECGSGAGACACDLCCSGFGCGTTSYDYGCP-RCQSCQCG--CGGGGGGVASIVS 81
D 7 ASAEQCGSGAGACACDLCCSGFGCGTTSYDYGCP-RCQSCQCG--CGGGGGGVASIVS 66
QY 82 RDLFERELLHRNDAAACLAGFYTYDAFLAAAGAFPAFTGDLTRKREVAFAFFQTSHE 141
D 67 SSMFDQMLKLRNDACQKGYFYNAFNAARSPFGFTSGDTTARKREIAAFAFFQTSHE 126
QY 142 TTGGWPTAPDGFSGYCFKQBGQSPSYCDQSDADWPCAPGKQYGRGPIQLTHNYNYP 201
D 127 TTGGWATAPDGFYANGYCWLRQGSFGDYCTPSGQWPCAPGKRYGRGPIQLTHNYNYP 186
QY 202 AGRATGVLLNPNLDVATDPTVAFKTAIFWMTTOSNKPSCHDVTGLWTPARDSAAGR 261
D 187 CGRATGVLLNPNLDVATDPTVAFKTAIFWMTTOSNKPSCHDVTGLWTPARDSAAGR 246
QY 262 VPGYGVITNINNGLECGRGTDVSRVQDRIGFYKRYCIIILGVSPGDLNDCGNORSFGNGL 320
D 247 LPFGFVITNINNGLECGRGTDVSRVQDRIGFYKRYCIIILGVSPGDLNDCGNORSFGNGL 305

RESULT 8

US-07-704-288C-6
; Sequence 6, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-6

Query Match 65.1%; Score 1167; DB 1; Length 310;

Best Local Similarity 67.2%; Pred. No. 7.1e-98;
Matches 201; Conservative 41; Mismatches 53; Indels 4; Gaps 3;

QY 25 ATAECGSGAGACACDLCCSGFGCGTTSYDYGCP-RCQSCQCG--CGGGGGGVASIVS 81
D 8 ASAEQCGSGAGACACDLCCSGFGCGTTSYDYGCP-RCQSCQCG--CGGGGGGVASIVS 67
QY 82 RDLFERELLHRNDAAACLAGFYTYDAFLAAAGAFPAFTGDLTRKREVAFAFFQTSHE 141
D 68 SSMFDQMLKLRNDACQKGYFYNAFNAARSPFGFTSGDTTARKREIAAFAFFQTSHE 127
QY 142 TTGGWPTAPDGFSGYCFKQBGQSPSYCDQSDADWPCAPGKQYGRGPIQLTHNYNYP 201
D 128 TTGGWATAPDGFYANGYCWLRQGSFGDYCTPSGQWPCAPGKRYGRGPIQLTHNYNYP 187
QY 202 AGRATGVLLNPNLDVATDPTVAFKTAIFWMTTOSNKPSCHDVTGLWTPARDSAAGR 261
D 188 CGRATGVLLNPNLDVATDPTVAFKTAIFWMTTOSNKPSCHDVTGLWTPARDSAAGR 246
QY 262 VPGYGVITNINNGLECGRGTDVSRVQDRIGFYKRYCIIILGVSPGDLNDCGNORSFGNGL 320
D 247 LPFGFVITNINNGLECGRGTDVSRVQDRIGFYKRYCIIILGVSPGDLNDCGNORSFGNGL 305

RESULT 9

US-08-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-6

Query Match 65.1%; Score 1167; DB 1; Length 310;

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; MOLECULE TYPE: protein
US-08-475-427-13

Query Match      63.7%; Score 1141.5; DB 2; Length 329;
Best Local Similarity 59.9%; Pred. No. 1.5e-95;
Matches 194; Conservative 54; Mismatches 69; Indels 7; Gaps 3;

QY 25 ATAEQGSQAGGAKADCLCCSFGCGTSDYCGP-RQSQCTG--CGGGGGVSIIVS 81
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 ASAEQGSQAGGAKARCCSFGWCGTNDYCGPNCQSQCPGGPTPPGGDLGSIIS 67
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 82 RDLFEFLHRNDACLAARFYIYDAPLAAGAPPAFGTTGDLDTKRREVAAPFGOTSHE 141
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 SSMFDQMLKRNNDACQKGFYSYNAFINAARSPFGTSGDTTARKREIAAFAAQTSH 127
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 142 TTGSGWAPDGPSTSWGKCFKQEGSPSYCDQADWPCAPKGYGRPIQLTHNYNGP 201
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 TTGWTATAPDGPYAWGVCWLRQSGSDYCTPSQWPCAPGRKYFGPQISHNYNGP 187
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 202 AGRAIGVLLNPDVATDPTVAFKTAINFWMTTQSNKPSCHDVITGLWPTARDSAGR 261
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 CGRAIGVLLNPDVATDPTVAFKTAINFWMTTQSNKPSCHDVITGLWPTARDSAGR 246
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 262 VPGYGVITNNGIECGMGQNDKVADRIQFYKYCDIFGIGYGNLDCYNOLSENVGL 320
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 LPQFGVITNNGIECGMGQNDKVADRIQFYKYCDIFGIGYGNLDCYNOLSENVGL 305

RESULT 10
US-08-475-427-13
; Sequence 13, Application US/08475427
; Patent No. 5859340
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Michel
; APPLICANT: GRISON, Rene
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: PIGNARD, Annie
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant gene coding for a protein
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475.427
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842.165
; FILING DATE: 01-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00607
; FILING DATE: 21-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90 09460
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/564/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 13:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-475-427-13

Query Match      63.7%; Score 1141.5; DB 2; Length 329;
Best Local Similarity 59.9%; Pred. No. 1.5e-95;
Matches 194; Conservative 54; Mismatches 69; Indels 7; Gaps 3;

QY 4 LRARCATAVLAVVLAATAECCGSGAGGAKADCLCCSFGCGTSDYCGP-RC 62
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRRTSKLITSLFSLVLLSALAONCGSGGKVCASGOCCKFCWCGNTNDHCGSGNC 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 QSQCTCGGGG---GGGYASIVSRDLFERLLHRNDACIAR-GFYTYDAFLAAGAFP 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 QSQCGGPGPGPVTTGGDLGVSINSFMDQMLKRNENSQCKNNFYSYNAFTAARSP 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 AFGTTGDLDTKRREVAAPFGTTSHTTGGWPTADGPFSGWYCYCFKQBGQSPSYCDQASD 176
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GFGTSGDINARKREIAAFAAQTSHETGGWPSAPDGFPAWGYCFLRGNPFGDYCSFSSQ 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 WPCAPGKOYYGRGPIQLTHNYNGPAGRAIGVLLNPDVATDPTVAFKTAINFWMTTQ 236
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 WPCAPGKRYGRGPIQLSHNYNGPAGRAIGVLLNPDVATDPTVAFKTAINFWMTPQ 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 237 SNKPSCHDVITGLWPTARDSAGRVPYGVITNNGIECGMGQNDKVADRIQFYKY 296
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 SPKPSCHDVITGRWNPAGDRSANRLEFGVITNNGIECGMGQNDKVADRIQFYKY 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 297 CDIFGIGYGNLDCYNOLSENVGL 320
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 CGILGVSPGDNLDCCGNQNSFGNGL 324

RESULT 11
US-08-475-427-13
; Sequence 13, Application US/07842165
; Patent No. 5932698
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Michel
; APPLICANT: GRISON, Rene
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: PIGNARD, Annie
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant gene coding for a protein
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/842.165
; FILING DATE: 19920501
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
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Db	192	ISWNINYQCGR	IGAIGVLLNKP	DLVATDSV	ISPKSLWFM	MTAQSPKPSH	VDTSRWT	251
QY	253	TARDAAAGRP	GVITNVING	IECGMGOND	KVADRGFKY	KYCDIFGIGY	CNNIDCYN	312
		:	:	:	:	:	:	
		:	:	:	:	:	:	
Db	252	SSDAARRLP	FGVTINII	NGLECGQDS	KVQDRIGF	KYCDLLGVG	YNNIDCY	311
QY	313	QLSFNVGL	320					
		:	:	:	:	:	:	
Db	312	QTPEGNSL	319					

RESULT 13
 US-07-704-288C-9
 ; Sequence 9, Application US/07704288C
 ; Patent NO. 5399680
 ; GENERAL INFORMATION:
 ; APPLICANT: LAMB, CHRISTOPHER J.
 ; APPLICANT: ZHU, QUN
 ; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
 ; TITLE OF INVENTION: ELEMENTS
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 90071-2921
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07704,288C
 ; FILING DATE: 22-MAY-1991
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P31 8899
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 546-4737
 ; TELEFAX: (619) 546-9392
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 318 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-07-704-288C-9

	Query Match	63.0%;	Score 1129;	DB 1;	Length 318;
	Best Local Similarity	63.6%;	Pred. No. 2e-94;		
	Matches 196;	Conservative	42;	Mismatches 68;	Indels 2;
					Gaps
Qy	13	LAVVLA AAAA V P T A T A E C G S Q G A G A K A C A L C S Q F G C G T T S D Y C G P R C Q S O C T C G G G	72		
Db	4	GVVVMLLLVGGSYGEQCGRAGGALCPGGNCQSQFCWCGSTTDYCGPCQSQCGSPSA	63		
Qy	73	GGGVASIVSRDLERFTLLHRNDACIALRGFTTYDAFLAAGAPAFGTGGDLDTRKREVA	13		
Db	64	PTDLSALISRSTPTDMLKLRNDGACPAKGYTTYDAFLAAAKYPSFGNTGDTATRKREIA	12		
Qy	133	AFFGQTSHETTGWPTADPGDFPNWGYCFKQEGSPSPSYCDQSADWFCAGKQYXGRPIQ	19		
Db	124	AFLGQTSHEITGGWATADPGDFYAWGYCFVBERN--PSTCSATPOFFCAPGQQYXGRPIQ	18		
Qy	193	LTHNMYNCPAGRAITGVDLLNNPOLVADPTVAFKTALFWMTTQSNKPSCHDVTGLWPT	25		

```

; LENGTH: 329 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-842-165-13

Query Match      63.7%; Score 1141.5; DB 2; Length 329;
Best Local Similarity 59.9%; Pred. No. 15e-95;
Matches 194; Conservative 54; Mismatches 69; Indels 7; Gaps 3;

Qy 4 LRACATAVLAVLVIAAAVTPATAEOGSGAGKACADCLCCSFGFCGTSYCGP-RC 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MRRTSKLTTFSLFLSVLLSAAALNQNGSGGGKVCASGCCSKFPGCGNTNDHCGSNC 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 63 QSQCCTGCGGG-----GGGVASIVSRDLFERLLHRNDAACILAR-GFTYDAFLAAAGFP 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 QSQCPGGGPGPGPYTGDLGSLVSNMFQDKLKHRENSCOGKKNFYSYNAFITAARSEP 120

Qy 117 AFGWTGDLDTKREVAFFGGTSHETTGWPTADPGPFSWGYCYKQEOGSPSYCDQSAD 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 GFGTSGDINAKRETAFAAFACTSHETTGWPSADPGPPAWGYCYFLRERNGPDYCSPSQ 180

Qy 177 WPCAPGKYGYGRGPITQLTHNTNYGFPAGRAIGVDLLNNPDLVATDPTVAFKTAIEWMTTQ 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 WPCAPGRKYFGFGTQISHNINYGCGRAIGVDLLNNPDLVATDPTVSEFKTAIEWMTTPQ 240

Qy 237 SNKPSCHDVITGLMTPTPARDSAAGRPVGYVLIINVGIEGCMQONDKVADRIGFYKRY 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 SPKPSCHDVITGRWNPAGDRSANPLPGFVTIININGLECGRDNDRKVRQDRIGFYRY 300

Qy 297 CDIFGIGYGNLDCYNQLSFNVGL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 CATTGVSPGNDLDCGNORSFGNGL 324
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 12
US-07-791-931-7
; Sequence 7, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791.931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Phaseolus vulgaris
US-07-791-931-7

Query Match 63.4%; Score 1135.5; DB 4; Length 328;
Best Local Similarity 63.6%; Pred. No. 5.3e-95;
Matches 196; Conservative 44; Mismatches 67;
Indels 1; Gaps 1;

```

QY	13	LAVLVAAAATPATAGCAQCGSAGAKACADCLCSQCFQCTTSDYCGPRCQCQCCTCGGG	72
Db	13	VGVWMLLVGSGYEQCGRQAGALCPGGNCSCQFGWCGSTTDCGPGCCQCGGPPA	72
QY	73	GGGVASIVSRDLFFERFLHRNDACLAGFYTYDAFLAAAGAPFAEFTGDLDTKRREVA	132
Db	73	PIDLGSLSIRSTFDQMLKHRNDGACPAGKYTYDAFLAAKAYPSGNTGDTATKRRETA	132
QY	133	AFEGTSHETTGWPATDPGFWSGYCFKQEGSPSPYCSQSDADWPCAPKQYVGRGPQ	192
Db	133	AFVQGTSHETTGWATADGYPANGYCFVRER-NPSYCSATPQFCAPGQQYVGRGPQ	191
QY	193	LTHNYNYPAGRAIGVGLNPNDLVADPTVAEKTALFWFMTQSNKPSCHDVITGLWTP	252

Db	182	ISWNYNGCGRAIGVDLLNKPDLVATDSVISFKSALWFMTAQSPKPSHSDVITSRWTP	241
QY	253	TARSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGYKRYCDIFGIGYGNLDCYN	312
Db	242	SSADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGRFKRYCDLLGVGYGNLDCYS	301
QY	313	QLSENVGL	320
Db	302	QTPFGNSL	309
RESULT 14			
US-08-379-259-9			
; Sequence 9, Application US/08379259			
; Patent No. 5695939			
; GENERAL INFORMATION:			
; APPLICANT: LAMB, CHRISTOPHER J.			
; APPLICANT: ZHU, QUN			
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT			
; TITLE OF INVENTION: DEFENSE REGULATORY			
; TITLE OF INVENTION: ELEMENTS			
; NUMBER OF SEQUENCES: 26			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK			
; STREET: 444 South Flower Street, Suite 2000			
; CITY: Los Angeles			
; STATE: California			
; COUNTRY: United States			
; ZIP: 90071-2921			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/379,259			
; FILING DATE:			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/704,288			
; FILING DATE: 22-MAY-1991			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Reiter, Stephen E.			
; REGISTRATION NUMBER: 31,192			
; REFERENCE/DOCKET NUMBER: P31 8899			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (619) 546-4737			
; TELEFAX: (619) 546-9392			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 9:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 318 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: unknown			
; TOPOLOGY: unknown			
; MOLECULE TYPE: protein			
US-08-379-259-9			
Query Match 63.0%; Score 1129; DB 1; Length 318;			
Best Local Similarity 63.6%; Pred. No. 2e-94;			
Matches 196; Conservative 42; Mismatches 68; Indels 2; Gaps 1;			
QY	13	LAVVLAATAATPATAEQCGSQAGKACDCLCGSQFGFCGTTSDYCGPRCQSQCTGGGG	72
Db	4	GVVWMLLVGGSYGECQGRAGGALCPGGNCCSQFQWCGSTTDYCGFGCQSQCGGSPA	63
QY	73	GGGVASTVSRDLFERLLHRNDAACLARGFTYDAFLAAAGAPFAFGTTGDLTRKREVA	132
Db	64	PTDLSALISRSTFDQMLKHRNDGACPAKGYTYDAFLAAAKAYPSFGNIGDTATRKREIA	123
QY	133	AFGQTSHTTGGWPTAPDGPFFSWGICYFKQEGSPPSYCDQSDADWPCAPGKQYIGRPIQ	192

Db	124	AFLGQTSHTTGGWATAPDGPYAWGYCFVBERN--PSTCSATPQFPCCAPGQOYVGRGPIQ	181
QY	193	LTNYNYGVPAGRAIGVDLLNKPDLVATDPTVAFKTALWFMTTQSNKPSCHDVTITGLWTP	252
Db	182	ISWNYNGCGRAIGVDLLNKPDLVATDSVISFKSALWFMTAGSPKPSHSDVITSRWTP	241
QY	253	TARSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGYKRYCDIFGIGYGNLDCYN	312
Db	242	SSADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGRFKRYCDLLGVGYGNLDCYS	301
QY	313	QLSENVGL	320
Db	302	QTPFGNSL	309
RESULT 15			
US-07-791-931-5			
; Sequence 5, Application US/07791931C			
; Patent No. 613507			
; GENERAL INFORMATION:			
; APPLICANT: Raikhel, Natasha V.			
; TITLE OF INVENTION: Nettle Lectin cDNA			
; FILE REFERENCE: MSU 4.1-114			
; CURRENT APPLICATION NUMBER: US/07/791,931C			
; CURRENT FILING DATE: 1991-11-12			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 5			
; LENGTH: 328			
; TYPE: PRT			
; ORGANISM: Solanum tuberosum			
US-07-791-931-5			
Query Match 62.8%; Score 1126; DB 4; Length 328;			
Best Local Similarity 62.7%; Pred. No. 3.8e-94;			
Matches 190; Conservative 48; Mismatches 61; Indels 4; Gaps 2;			
QY	22	VTPATAEQCGSQAGKACDCLCGSQFGFCGTTSDYCGP-RCQSQCTGG---GGGGVA	77
Db	21	VSAALAQNCGSGGGKACASGQCSKFGWCGNTNDYCGSGNCQSQCPGGGPGFGGDLG	80
QY	78	SIVSRDLFERLLHRNDAACLARGFTYDAFLAAAGAPFAFGTTGDLTRKREVAFFGQ	137
Db	81	SAISNMFQMLKHRNENSCQGNFYNAFINAARSFFGFGTSGDINARKREIAFFAQ	140
QY	138	TSHTTGGWPTAPDGPFSWGYCFKQCGSPPSYCDQSDADWPCAPGKQYIGRPIQLTHNY	197
Db	141	TSHTTGGWASAPDGPYAWGYCFLRERGNPDYCPSPSQWPCAPGKRYFGRGPIQISHNY	200
QY	198	NYGPAGRAIGVDLLNKPDLVATDPTVAFKTALWFMTTQSNKPSCHDVTITGLWTPTRDS	257
Db	201	NYGPCGRAIGVDLLNKPDLVATDFVISFTALWFMTTQSNKPSCHDVTITGRNPSADR	260
QY	258	AAGRVPGYGVITNVINGGIECGMGQNDKVADRIGYKRYCDIFGIGYGNLDCYNOLSN	317
Db	261	AANRLPGYGVITNVINGGLECGRGTDNRVQDRIGFGRYRYSILGVTGPDNLDCVNORWEG	320
QY	318	VGL	320
Db	321	NAL	323
Search completed: May 3, 2002, 18:43:04			
Job time: 747 sec			

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 18:32:10 ; Search time 88.01 Seconds
(without alignments)
279.563 Million cell updates/sec

Title: US-09-534-229C-2
Perfect score: 1792
Sequence: 1 MSTLRARCAVLAVALAA.....YGNLDCYNQLSFNVGLAAQ 323
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330	74.2	339	2 S39979	chitinase (EC 3.2.
2	1326.5	74.0	340	2 S40414	chitinase (EC 3.2.
3	1315	73.4	302	2 JC2071	chitinase (EC 3.2.
4	1297	72.4	318	2 T04403	probable chitinase
5	1287.5	71.8	332	2 T04484	probable chitinase
6	1283	71.6	320	2 S38670	chitinase (EC 3.2.
7	1272	71.0	335	2 T03239	probable chitinase
8	1238.5	69.1	323	2 T03614	chitinase (EC 3.2.
9	1230	68.6	336	2 S15997	chitinase (EC 3.2.
10	1218	68.0	318	2 S14948	chitinase (EC 3.2.
11	1196.5	66.8	324	2 S56694	chitinase (EC 3.2.
12	1193	66.6	318	2 S65019	chitinase (EC 3.2.
13	1192	66.5	322	2 S54806	chitinase (EC 3.2.
14	1187.5	66.3	311	2 T07838	chitinase (EC 3.2.
15	1185	66.1	322	1 S37344	chitinase (EC 3.2.
16	1184	66.1	324	2 S20981	chitinase (EC 3.2.
17	1181	65.9	329	2 S08627	chitinase (EC 3.2.
18	1177	65.7	318	2 S43317	chitinase (EC 3.2.
19	1174	65.5	316	2 S65020	chitinase (EC 3.2.
20	1173.5	65.5	319	2 JC2252	chitinase (EC 3.2.
21	1168	65.2	327	2 T09687	chitinase (EC 3.2.
22	1163	64.9	324	2 T10802	chitinase (EC 3.2.
23	1154	64.4	335	2 B45511	chitinase (EC 3.2.
24	1149.5	64.1	321	2 S57482	chitinase class 1
25	1146	64.0	322	2 S59953	chitinase (EC 3.2.
26	1145.5	63.9	320	2 S59947	chitinase (EC 3.2.
27	1144.5	63.9	334	2 S20982	chitinase (EC 3.2.
28	1143	63.8	302	2 T10810	chitinase (EC 3.2.
29	1130.5	63.1	327	1 JQ0965	chitinase (EC 3.2.

ALIGNMENTS

RESULT 1

S39979
chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S39979
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice
A:Reference number: S39979; MUID:94049667
A:Accession: S39979
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <NIS>
A:Cross-references: EMBL:X56787
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:91-329/Domain: plant chitinase homology <PCH>

Query Match		74.2%	Score 1330;	DB 2;	Length 339;
Best Local Similarity		71.4%	Pred. No. 1.4e-94;		
Matches		242;	Conservative	29;	Mismatches 52; Indels 16; Gaps 3;
QY	1	MSTLR-----ARCATAVLAVLVAAAVTPATAECGSGAAGKACDCLCCSQFGCGTTS	55		
Db	1	MSTPRAASLAKKALAVLAAALATAARAECQAAGAGCPNCLCCSRWCGTTS	60		
QY	56	DYCGPRCSQCTGG-----GGGGVASTVSRDLERFLHRNDAACLARGFTYDAF	108		
Db	61	DFCGDGGCGSGCGGPTTPPSPSDGVGSIVPRDLERLLHRNDGCPARGFTYDAF	120		
QY	109	LAAGAPFAFTGDLTKREVAFFGQTSHETGWTAPDGFPSWGYCFKQEGSGPP	168		
Db	121	LAARAPFAFGTNTETKREVAFLGQTSHEITGWTAPDGFPSWGYCFKQEQNPPS	180		
QY	169	SYCQSDAWPCAPKQYGRGPIQLTHNYNGPAGRAIGVLLNPNPDVATDPVAKTA	228		
Db	181	DYCPSPSPWPAPGRKYYGRGPIQLSFNFNYPAGRAIGVLLNPNPDVATDVSFKTA	240		
QY	229	1WFWMVTQSNKPSCHDVTGLWTPARDAAAGRVGYVITNVIINGGLECGMGNDKVD	288		
Db	241	1FWMTPOGNKPSHDVITGRWAPSPADAAAGRAPGYVITNVIINGGLECGHGFDDRVAN	300		
QY	289	RIGFYKRYCDIFGIGNNLDYCNOLSFN----VGLAAQ	323		
Db	301	RIGFYRCGAFGIGTGNLDYCNORPENSGLAEQ	339		

RESULT 2
S40414

chitinase (EC 3.2.1.14) - rice
 C:Species: Oryza sativa (rice)
 C>Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S40414
 R:Nishizawa, Y.
 submitted to the EMBL Data Library, November 1990
 A:Reference number: S40414
 A:Accession: S40414
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-340 <NLS>
 A:Cross-references: EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407472
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:33-74/Domain: hevein chitin-binding domain homology <HCB>
 F:92-330/Domain: plant chitinase homology <PCH>

Query Match 74.0%; Score 1326.5; DB 2; Length 340;
 Best Local Similarity 70.9%; Pred. No. 2.6e-94;
 Matches 241; Conservative 29; Mismatches 53; Indels 17; Gaps 3;

QY 1 MSTLRARCATA-----VLAVLAAAVTPATAEQGSGAGKACADCLCCSQFGCGTTS 55
 DB 1 MSTPRAASTAKKAAALVALAVLAAALAAARAEQGAQAGARCNCLCCSRWGCPTTS 60
 QY 56 DYCPGRCQCTGCG-----GGGGVAVISGRDLFERLLHRNDAACLAGFYTYDA 107
 DB 61 DFCGDCGSCSGCGPTPTPPSPDSGVSIVPRDLFERLLHRNDGACPARFYIYEA 120
 QY 108 FLAAGAPFAGTGGDLTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEGSP 167
 DB 121 FLAAAAAPFAPGGTGTETRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEQNP 180
 QY 168 PSYDQSDWPCAPGKQYGRPIQLTHNYNGPAGRAIGVDLLNPDVATDTPVAFKT 227
 DB 181 SDYQSPFPCAPGKRYGRPIQLSFNFNGPAGRAIGVDLLNPDVATDTPVAFKT 240
 QY 228 ALFWMTTQSNKPSCHDVITGLWPTARDSAAGRPYGVITNVINGIEGGMGNDKVA 287
 DB 241 ALFWMTTQGNKPSHSHVITGRWAPSPADAAAGRAPGYGVITNVINGLEGHGPDRA 300
 QY 288 DRIGFYKRYCDIFGIGYGNLDYCNLSFN-----VGLAAQ 323
 DB 301 NRIGFYRYCGAFGTGTGNLDYCNORPFSNSSVGLAEQ 340

RESULT 3
 JC2071
 chitinase (EC 3.2.1.14) a - rye
 C:Species: Secale cereale (rye)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
 C:Accession: JC2071
 R:Yamagami, T.; Funatsu, G.
 Biosci. Biotechnol. Biochem. 58, 322-329, 1994
 A:Title: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale
 Cereale)
 A:Reference number: JC2071; MUID:94169514
 A:Accession: JC2071
 A:Molecule type: protein
 A:Residues: 1-302 <YAM>
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-42/Domain: hevein chitin-binding domain homology <HCB>
 F:64-302/Domain: plant chitinase homology <PCH>

Query Match 73.4%; Score 1315; DB 2; Length 302;
 Best Local Similarity 76.1%; Pred. No. 3.8e-93;
 Matches 229; Conservative 24; Mismatches 36; Indels 12; Gaps 1;

QY 28 EQCGSAGGACADCLCCSQFGTSDYCGPRCSQCTGCG-----GGGG 75
 DB 1 EQCGSAGGATCNCCLCCSRFGWCGSTSDYCGDCGCSQACGCGGGTPTPTPTPSGGG 60

QY 76 VASIVSRDLFERLLHRNDAACLAGFYTYDAFLAAAGAPFAGTGGDLTRKREVAFF 135
 DB 61 VSSIVSRALFDRMLLRNDGACQAKGFYTYDAFVAAAGAPFGTGTSTDRKREVAFL 120
 QY 136 GQTSHTTGGWPTAPDGPFSWGYCFKQEGSPSYCSQSDWPCAPGKQYGRPIQLTH 195
 DB 121 AQTSHTTGGWATPDGAFAGWGYCFKQERGATSNICYTFSQAQWPCAPGKSYGRPIQLSH 180
 QY 196 NYNGPAGRAIGVDLLNPDVATDTPVAFKTAIFWMTTQSNKPSCHDVITGLWPTAR 255
 DB 181 NYNGPAGRAIGVDLLNPDVATDTPVSKTAMFWMTAQAPKPSHAVITGOWSPSGT 240
 QY 256 DSAAGRPYGVITNVINGIEGGMGNDKVAADRIGFYKRYCDIFGIGYGNLDYCNLS 315
 DB 241 DRAAGRPYGVITNVINGIEGGMGNDKVAADRIGFYKRYCDILGVGYNLDYCNQRP 300
 QY 316 F 316
 DB 301 F 301

RESULT 4
 T04403
 probable chitinase (EC 3.2.1.14) precursor - barley
 C:Species: Hordeum vulgare (barley)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
 C:Accession: T04403
 R:Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
 submitted to the EMBL Data Library, September 1993
 A:Description: Isolation and characterization of a barley chitinase genomic clone.
 A:Reference number: Z15336
 A:Accession: T04403
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-318 <IGN>
 A:Cross-references: EMBL:U02287; NID:g495304; PIDN:AAAL8586.1; PID:g495305
 A:Experimental source: cv. NK1558
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-318/Product: chitinase #status predicted <MAT>
 F:20-60/Domain: hevein chitin-binding domain homology <HCB>
 F:80-318/Domain: plant chitinase homology <PCH>

Query Match 72.4%; Score 1297; DB 2; Length 318;
 Best Local Similarity 74.0%; Pred. No. 4.4e-92;
 Matches 233; Conservative 27; Mismatches 43; Indels 12; Gaps 3;

QY 12 VLAVLAAAVTPATAEQGSGAGKACADCLCCSQFGTSDYCGPRCSQCTGCG 71
 DB 5 VLFVAVMAAA-TMAVEQCGSQAGGATCNCCLCCSRFGWCGST-PYCGDGCQSCSGCG 62
 QY 72 -----GGGVASIVSRDLFERLLHRNDAACLAGFYTYDAFLAAAGAPFAGT 121
 DB 63 GSTPTPTPSGGGVSSIVSRALFDRMLLRNDGACQAKGFYTYDAFVAAASAFKGT 122
 QY 122 GLDTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEGSPSYCSQSDWPCAP 181
 DB 123 GQTDTRKREVAAPFAGTSHETTGGWATPDGAFAGWGYCFKQERGATSNICYTSPSAQWPCAP 182
 QY 182 GKQYGRPIQLTHNYNGPAGRAIGVDLLNPDVATDTPVAFKTAIFWMTTQSNKPS 241
 DB 183 GKSYGRPIQLSHNYNGPAGRAIGVDLLNPDVATDTPVSKTAMFWMTAQAPKPS 242
 QY 242 CHDVITGLWPTARDSAAGRPYGVITNVINGIEGGMGNDKVAADRIGFYKRYCDIFG 301
 DB 243 SHAVITGOWSPSGTDRAGRPVFGVITNVINGIEGGMGNDKVAADRIGFYKRYCDIFG 302
 QY 302 IGYGNLDYCNLSF 316
 DB 303 VGYGNLDYCSQRPF 317


```
RESULT 5
T04484
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T04484
R:Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
A:Title: Identification of an enhancer/silencer sequence directing the aleurone-specific
A:Reference number: Z15373; MUID:95078949
A:Accession: T04484
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-332 <LEA>
A:Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961
C:Genetics:
A:Gene: CH133
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:28-69/Domain: hevein chitin-binding domain homology <HCB>
F:85-322/Domain: plant chitinase homology <PCH>

Query Match 71.8%; Score 1287.5; DB 2; Length 332;
Best Local Similarity 71.0%; Pred. No. 2.4e-91;
Matches 230; Conservative 35; Mismatches 44; Indels 15; Gaps 4;

QY 11 AVLAIVLAAAVTP--ATAECGSGAAGKACDCLCCSGFCGTTSDYCGPCGSOCTG 68
DB 9 AIVAILVLAALAAVYRAOCQSGAGGATPCNCLCCSKFSGTSDYCGAGCQSCG 68
QY 69 CG-----GGGGVASIVSRDLERFLHRLN--DAACLAGFTYDAFLAAAGAFPAFG 119
DB 69 CGPTPPGSPGGVSSILSRDLERFLHRLNRCQDA--GFTYDAFLAAATFPAG 124
QY 120 TGDLTRKREVAFAFGCTSHETGGWPTAPDPFSGWYCFKQEGSPSPYCDQSDAWPC 179
DB 125 TTGSTETKQVAAFFGCTSHETGGWATAPDPGYSGWYCFKQEGSPSPYCDQSDAWPC 184
QY 180 APGQYGRGPQIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNK 239
DB 185 VQDQYIGRGFIMLSWNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNK 244
QY 240 PSCHVITGLWPTARDAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDI 299
DB 245 PSSHAVITGWTPTAADTAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCNI 304
QY 300 FGIGYGNLDCYNQLSFNVGLAAQ 323
DB 305 LGVGYGNLDCYNQRPVEGLLIQ 328

RESULT 6
S38670
Chitinase (EC 3.2.1.14) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Jun-1999
C:Accession: S38670
R:Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reisener, H.J.
A:Title: Identification of an enhancer/silencer sequence directing the aleurone-specific
A:Reference number: Z15373; MUID:95078949
A:Accession: S38670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <LIA>
A:Cross-references: EMBL:X76041; NID:g416028; PIDN:CAA53626.1; PID:g416029
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-320/Domain: plant chitinase homology <PCH>
```

```
Query Match 71.6%; Score 1283; DB 2; Length 320;
Best Local Similarity 70.5%; Pred. No. 5.2e-91;
Matches 222; Conservative 34; Mismatches 49; Indels 10; Gaps 1;

QY 12 VLAVLAAAVTATATOCGSGAAGKACDCLCCSGFCGTTSDYCGPCGSOCTGCGG 71
DB 5 VVAMLAFAFAVAHAHQCGSGAGGATPCNCLCCSKFSGTSDYCGNGCQSCGCG 64
QY 72 G-----GGGVASIVSRDLERFLHRLNDAACLAGFTYDAFLAAAGAFPAFGTT 121
DB 65 GGPVPVPTTGGVSSILSRDLERFLHRLNDAACLAGFTYDAFLAAAGAFPAFGTT 124
QY 122 GDLTRKREVAFAFGCTSHETGGWPTAPDPFSGWYCFKQEGSPSPYCDQSDAWPCAP 181
DB 125 GGADVRKREVAFAFGCTSHETGGWPTAPDPGYSGWYCFKQEGSGAASDYSNQPWPCAP 184
QY 182 GKQYGRGPQIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNKPS 241
DB 185 GKRYFGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNKPS 244
QY 242 CHDVITGLWPTARDAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDIFG 301
DB 245 SHDVITGRWSPSGADQAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDILG 304
QY 302 IGYGNLDCYNQLSF 316
DB 305 VTYGNLDCYNQRPF 319

RESULT 7
T03239
probable chitinase (EC 3.2.1.14) precursor - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000
C:Accession: T03239
R:Anuratha, C.S.; Mew, T.; Muthukrishnan, S.
A:Title: Induction of chitinases and beta-glucanases in Rhizoctonia solani infe
A:Reference number: Z14854
A:Accession: T03239
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-335 <ANU>
A:Cross-references: EMBL:U02286; NID:g495302; PIDN:AAAL8585.1; PID:g495303
A:Experimental source: leaf, strain IR58
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-335/Product: chitinase #status predicted <MAT>
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:90-325/Domain: plant chitinase homology <PCH>
```

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Query Match 71.0%; Score 1272; DB 2; Length 335;
Best Local Similarity 70.1%; Pred. No. 3.8e-90;
Matches 237; Conservative 27; Mismatches 56; Indels 18; Gaps 6;

QY 1 MSTLRARCATA-----VLAVLAAAVTATATOCGSGAAGKACDCLCCSGFCGTT 55
DB 1 MSTPRAASLAKKAALVALAVLAAALATAACAEQCGAAGGARGARPCNCLCCSRWGCST 60
QY 56 DYCGPCGSOCTGCG-----GGGGVASIVSRDLERFLHRLNDAACLAGFTYDAFL 109
DB 61 DFCGDCGSCGSCGCTPTTPSPSGVGSIVPRDLERFLHRLNDAACLAGFTYDAFL 120
QY 110 AAGAFPAFGTTGDLTRKREVAFAFGCTSHETGGWPTAPDPFSGWYCFKQEGSPSPS 169
DB 121 RRA-AFPAPGGTGTETKREVAFAFGCTSHETGGWPTAPDPFSGWYCFKQEGNPPSD 179
QY 170 YCDQSDAWPCAPGKQYGRGPQIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAI 229
DB 180 YCQFAGWPCAPGRKYGRGPQIQLSFNFNGPAGRAIGVDLLSNPLVATDPTVAFTAI 239
```

QY 230 WFWMTQSNKPSCHDVTGLWTPETARDSAAGRVPGYGVITNVINGIECGMGQNDKVADR 289
Db 240 WFWMTQSNKPSCHDVTGRWAP-RDVAAGRA-GGVITNVINGIECGMGQNDKVADR 297
QY 290 IGFYKRYCDIFGIGYGNNDYCNQISFN----VGLAAQ 323
Db 298 IGFYQAYCAGAFGIGTGNLDYCNQRFNSGSSVGLAEQ 335
RESULT 8
T03614
chitinase (EC 3.2.1.14) - rice
N:Alternate names: endochitinase
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03614
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice chitinase gene
A:Reference number: S39979; MUID:94049667
A:Accession: T03614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-323 <NIS>
A:Cross-references: EMBL:D16221; NID:g452232; PIDN:BAA03749.1; PID:g500615
A:Experimental source: cv. Nipponbare
C:Genetics:
A:Gene: Cht-1
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
C:Keywords: glycosidase; hydrolase
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-322/Domain: plant chitinase homology <PCH>
Query Match 69.1%; Score 1238.5; DB 2; Length 323;
Best Local Similarity 69.3%; Pred. No. 1.3e-87;
Matches 224; Conservative 31; Mismatches 51; Indels 17; Gaps 4;
QY 9 ATAVLAVVLAATAVPATACQSGAGGAKCADCLOCSQFQCGTTSQDYCGPRCQSOCTG 68
Db 3 ALAVV-VVATAFVAVVAVRGQCSQAGGALCPNCLCCSQYGCWGCTSAICGSCQCSG 61
QY 69 -----CGGGGGGVASIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAAGAFPAF 118
Db 62 SCGGGPTPSSGGGGGVASIVSRDLFQDMLHRNDAAACPAKFNFTYDAFLAAAGAFPSF 121
QY 119 GTTGLDTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEQ----GSPPSYCDQS 174
Db 122 ATTGDAATRKREVAAPFLAQTSHETTGWATAPDGPYSWGVCYCFKEENNGNYGS--DYCVQS 179
QY 175 ADWPCAPGKQYGRGPTQLTHNINYPAGRAIGVDLNNPDVATDPTVAFKTAIFWMT 234
Db 180 SQWPCAAGKYYGRGPIQISYNYNYPAGQAIGSNLLSPDLVADATVSKTAFWFMT 239
QY 235 TQSNKPSCHDVITGLWTPETARDSAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYK 294
Db 240 POSPKPSCHAVMTGQWTPNGNDQAAGRVPGYGVITNVINGIECGMGADSRVADRIGFYK 299
QY 295 RYCDIFGIGYGNLDYCNQISFN 317
Db 300 RYCDMLGVSYGANLDCYNQRFN 322
RESULT 9
S15997
chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S15997
R:Zhu, Q.; Lamb, C.J.
Mol. Gen. Genet. 226, 289-296, 1991
A:Title: Isolation and characterization of a rice gene encoding a basic chitinase.

A:Reference number: S15997; MUID:91238706

A:Accession: S15997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <MOL>
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:22-63/Domain: hevein chitin-binding domain homology <HCB>
F:81-320/Domain: plant chitinase homology <PCH>

Query Match 68.6%; Score 1230; DB 2; Length 336;
Best Local Similarity 69.3%; Pred. No. 6.2e-87;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;
QY 4 LRARCATAVLAVVLAATAVPATACQSGAGGAKCADCLOCSQFQCGTTSQDYCGPRCQ 63
Db 1 MRALAVVAVVAVRGQCSQAGGALCPNCLCCSQYGCWGCTSDYCGAGQ 57
QY 64 SOCT-----CGGGGGGVASIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAAGAF 115
Db 58 SQCSRLRRRRPDASGGGGGVASIVSRSLFDMLHRNDAAACPASNFYTYDAFVAASAF 117
QY 116 PAFGTTGDLTTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
Db 118 PGFAAAGADATNKRVAAPFLAQTSHETTGWATAPDGPYSWGVCYCFKEENGAGPDYCCQS 177
QY 175 ADWPCAPGKQYGRGPTQLTHNINYPAGRAIGVDLNNPDVATDPTVAFKTAIFWMT 234
Db 178 AQPKPCAGKYYGRGPIQISYNYNYPAGQAIGADLLGDPDLVADATVSKTAFWFMT 237
QY 235 TQSNKPSCHDVITGLWTPETARDSAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYK 294
Db 238 POSPKPSCHAVMTGQWTPNGNDQAAGRVPGYGVITNVINGIECGMGADSRVADRIGFYK 297
QY 295 RYCDIFGIGYGNLDYCNQ 313
Db 298 RYCDMLGVSYGANLDCYSQ 316

RESULT 10
S14948
chitinase (EC 3.2.1.14) - rice
N:Alternate names: class I endochitinase
C:Species: Oryza sativa (rice)
C:Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C:Accession: S14948
R:Huang, J.K.; Wen, L.; Swegle, M.; Tran, H.C.; Thin, T.H.; Naylor, H.M.; Muthukrishn
Plant Mol. Biol. 16, 479-480, 1991
A:Title: Nucleotide sequence of a rice genomic clone that encodes a class I endochiti
A:Reference number: S14948; MUID:91370895
A:Accession: S14948
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <HUA>
A:Cross-references: EMBL:X54367; NID:g20195; PIDN:CAA38249.1; PID:g20196
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:19-60/Domain: hevein chitin-binding domain homology <HCB>
F:79-316/Domain: plant chitinase homology <PCH>

Query Match 68.0%; Score 1218; DB 2; Length 318;
Best Local Similarity 70.1%; Pred. No. 4.9e-86;
Matches 218; Conservative 31; Mismatches 50; Indels 12; Gaps 5;
QY 13 LAVVLAATAVPATACQSGAGGAKCADCLOCSQFQCGTTSQDYCGPRCQSOCT-GCG- 70
Db 4 LALAVVAVVAVRGQCSQAGGALCPNCLCCSQYGCWGCTSDYCGAGCQSCGCGG 63
QY 71 -----GGGGGVASIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAAGAFPGTTGD 123
Db 64 GTPPPSGGGGVASIIISPSLFDQMLHRNDQAACRAKGFYTYDAFVAANAYPDFATRD 123


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QY 68 -----CCGGGGVAVISRDLEFRLHNRNDAACLAGFYTYDAFLAAGAFPAF 118
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 QLRRRDRPSGGGGVAVISVRSFQMLHNRNDAACPAKMLTYDAFVAANAFPTF 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 119 GTGDLDTKRREVAFAAFQGTSHETTGWTPADPGPSWGYCFKQEQ----GSPSPCDQS 174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 ATTGDAIRKREVAFAAFLAQSHTMGWATADPGPSWGYCFKRENNNGVS--DYCVQS 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 ADWPCAPKQYGRGPQLQHLNHNYPAGRAIGVDLLNPNLDVATDPTVAFKTAIFWMT 234
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 180 SQWPCFACRAGKYGRGPQISYNTNYPAGAGISNLLSNPD-ASDATVSGFKTAFWMT 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 TQSNKPSCHDVITGLWPTTARDAAAGRVPGYGVITNVINGIECGMGONDKVADRIGFYK 294
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 PQSEKPSCHAVMTGQWTPNGNDQAAGRVPGYGVVTVINGVECGHGADSRVADRIGFYK 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 RYCDIFGIGYGNLDCYNQLSFN 317
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 RYCDMLGVSYGANLDCYNQRPFN 321
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 14

T07838

chitinase (EC 3.2.1.14) - cucurbit

C;Species: Cucurbita sp. (cucurbit)

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000

C;Accession: T07838

R;Saaka, M.

submitted to the EMBL Data Library, June 1998

A;Reference number: Z16165

A;Accession: T07838

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-311 <S>A>

A;Cross-references: EMBL:AB015655; PIDN:PAA31131.1

C;Genetics:

A;Gene: chitp1

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;20-61/Domain: hevein chitin-binding domain homology <HCB>

F;75-311/Domain: plant chitinase homology <PCH>

```
Query Match          66.3%; Score 1187.5; DB 2; Length 311;
Best Local Similarity 69.0%; Pred. No. 1e-83;
Matches 211; Conservative 31; Mismatches 59; Indels 5; Gaps 2;
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QY 15 VVLAATAVPATACQSGOAGKACDCLCSOFGCGTTSYDYGCP-RCOSQCTGCGGG 70
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7  IVLAFVFLGAABEQCGRQANGALCPNRLCCSQFGWCGTDEYCKNNCQSOCTPFSTGGG 66
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 GGGGGVAVISRDLEFRLHNRNDAACLAGFYTYDAFLAAGAFPAFTGDLDTKRRE 130
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 GGGGSGVSIINEALYNQMLKYSKDPKPCPSNGFYRYNAFITAAQSFSGFTGDAATKRRE 126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 131 VAAFFGQTSHTTGGWTPADPGPSWGYCFKQEQGSPSPSYCDQSADWPCAPGKQYGRGP 190
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 127 LAAFFGQTSHTTGGWATADPGPYAWGYCFTRER--NQDVCYCPNQOQWPCAAGQKYGRGP 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 191 TQLTHNYPAGRAIGVDLLNPNLDVATDPTVAFKTAIFWMTTQSNKPSCHDVITGLW 250
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TQLTHNYPAGRALNUNLNNLDVATDPTVAFKTAIFWMTTQSNKPSCHDVITGRW 245
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 251 TPTARDSAAGRVPGYGVITNVINGIECGMGONDKVADRIGFYKRYCDIFGIGYGNLDC 310
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 246 QPSAADSAAAGRVPGYGVITNVINGIECGRGADSRVADRIGFYKRYCDLLGIGYGNLDC 305
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 311 YNQLSF 316
      |||||
Db 306 NNQRSF 311
```

RESULT 15

S37344

chitinase (EC 3.2.1.14) chi9 precursor - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: S37344; S38838; S25637

R;Danthash, N.; Wagenmakers, C.A.M.; van Kan, J.A.L.; de Wit, P.J.G.M.

Plant Mol. Biol. 22, 1017-1029, 1993

A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporium

A;Reference number: S37341; MUID:94003061

A;Accession: S37344

A;Molecule type: mRNA

A;Residues: 1-322 <DAN>

A;Cross-references: EMBL:Z15140; NID:g19190; PIDN:CAA78845.1; PID:g19191

A;Accession: S38838

A;Molecule type: protein

A;Residues: 23-42;202-216;224-236;247-258 <DAN>

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-322/Product: chitinase chi9 #status experimental <MAT>

F;23-65/Domain: hevein chitin-binding domain homology <HCB>

F;75-314/Domain: plant chitinase homology <PCH>

```
Query Match          66.1%; Score 1185; DB 1; Length 322;
Best Local Similarity 66.1%; Pred. No. 1.6e-83;
Matches 203; Conservative 41; Mismatches 61; Indels 2; Gaps 2;
```

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QY 16 VLAATAVPATACQSGOAGKACDCLCSOFGCGTTSYDYGCP-RCOSQCTGCGGG 74
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 LLFSVLLLSASAEQCGSQAGCALCSGKCSKFGWCGNTINEYCGNGCQSCQCGGPGPSG 70
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 75 GVASIVSRDLFERFLHNRNDAACLAGFYTYDAFLAAGAFPAFTGDLDTKRREVA 133
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 71 DLGGVINSDFQMLHNRNDAACQGNFYNAFVTAAGFPCTGTDITAKREIAA 130
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 134 FFGQTSHTTGGWTPADPGPSWGYCFKQEQGSPSPSYCDQSADWPCAPGKQYGRGP 193
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 FLAQTSHETTGWTPADPGPYAWGYCFLEQSGSPDYCTPSSQWPCAPGKRYFGRP 190
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 194 THNYPAGRAIGVDLLNPNLDVATDPTVAFKTAIFWMTTQSNKPSCHDVITGLW 253
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 SHNTNYGFCGRAIGVDLLNPNLDVATDPTVAFKTAIFWMTTQSNKPSCHDVITGRW 250
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 254 ARDSAAAGRVPGYGVITNVINGIECGMGONDKVADRIGFYKRYCDIFGIGYGNLDC 313
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 GADQAANRVPGYGVITNVINGIECGHGSDSRVQDRIGFYRYCYGILLGSPENLDCGN 310
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 314 LSFNVGL 320
      |||||
Db 311 RSFGNGL 317
```

Search completed: May 3, 2002, 18:32:12

Job time: 7475 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:48:31 ; Search time 78.59 Seconds
(without alignments)

150.690 Million cell updates/sec

Title: US-09-534-229c-2

Perfect score: 1792

Sequence: 1 MSTLRARCATAVLAVLAAA.....YGNLDCYNOLSPNVGLAAQ 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1297	72.4	318	1	CHT1_HORVU
2	1320	68.6	336	1	CHT2_ORYSA
3	1218	68.0	318	1	CHT1_ORYSA
4	1196.5	66.8	324	1	CHT2_PEA
5	1193	66.6	318	1	CHT1_SOLTU
6	1185	66.1	322	1	CHT1_LYCES
7	1184	66.1	324	1	CHT2_TOBAC
8	1181	65.9	329	1	CHT1_TOBAC
9	1177	65.7	318	1	CHT3_SOLTU
10	1174	65.5	316	1	CHT2_SOLTU
11	1166	65.1	321	1	CHT1_THECC
12	1163	64.9	324	1	CHT1_GOSHI
13	1154	64.4	322	1	CHT1_ARATH
14	1146	64.0	322	1	CHT2_BRANA
15	1145.5	63.9	320	1	CHT2_PEA
16	1144.5	63.9	334	1	CHT3_TOBAC
17	1143	63.8	302	1	CHT2_GOSHI
18	1139	63.6	314	1	CHT2_VITVI
19	1135.5	63.4	328	1	CHT1_PHAVU
20	1130.5	63.1	327	1	CHT5_PHAVU
21	1126	62.8	328	1	CHT7_SOLTU
22	1106	61.7	302	1	CHT4_SOLTU
23	1055	58.9	266	1	CHT2_HORVU
24	1010	56.4	340	1	CHT6_POPTR
25	954	53.2	246	1	CHT1_LYCES
26	867	48.4	303	1	CHT1_POPTR
27	826.5	46.1	247	1	CHT1_LYCES
28	818.5	45.7	254	1	CHT1_PETHY
29	817	45.6	253	1	CHT1_TOBAC
30	784	43.8	253	1	CHT1_TOBAC
31	781.5	43.6	253	1	CHT1_LYCCI
32	766.5	42.8	253	1	CHT1_LYCES
33	765	42.7	316	1	CHT8_POPTR

RESULT 1

ID	CHT1_HORVU	STANDARD;	PRT;	318 AA.
AC	P11955;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	26 KDA ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. NK 1558; TISSUE=Leaf;			
RA	Ignatius S.M.J., Huang J., Muthukrishnan S.;			
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 141-318 FROM N.A.			
RC	STRAIN=CV. HIMALAYA;			
RA	Swegle M., Huang J.-K., Lee G., Muthukrishnan S.;			
RT	"Identification of an endochitinase cDNA clone from barley aleurone cells."			
RT	Plant Mol. Biol. 12:403-412(1989).			
CC	FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN			
CC	CONTAINING FUNGAL PATHOGENS.			
CC	CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF			
CC	N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.			
CC	INDUCTION: BY ETHYLENE.			
CC	SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO			
CC	CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL			
CC	CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL			
CC	HYDROLASES).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to licensed@isb-sib.ch).			
CC	EMBL; U02287; AAA18586.1; -			
DR	EMBL; X15349; CAA33407.1; -			
DR	PIR; S04131; S04131.			
DR	HSSP; P23951; 2BAA.			
DR	InterPro; IPR001002; Chitin_bind.			
DR	InterPro; IPR000726; Glyco_hydro_19.			
DR	Pfam; PF00187; chitin_binding; 1.			
DR	Pfam; PF00182; Glyco_hydro_19; 1.			
DR	PRINTS; PR00451; CHITINBINDNG.			
DR	ProDom; PD000574; Glyco_hydro_19; 1.			
DR	ProDom; PD000609; Chitin_bind; 1.			
DR	SMART; SM00270; ChtBD1; 1.			
DR	PROSITE; PS00773; CHITINASE_19_1; 1.			

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DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 318 26 KDA ENDOCHITINASE 1.
FT DOMAIN 20 62 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 22 37 BY SIMILARITY.
FT DISULFID 31 43 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 53 57 BY SIMILARITY.
SQ SEQUENCE 318 AA; 33402 MW; 42D62B2FE8041954 CRC64;

Query Match 72.4%; Score 1297; DB 1; Length 318;
Best Local Similarity 74.0%; Pred. No. 3.2e-92;
Matches 233; Conservative 27; Mismatches 43; Indels 12; Gaps 3;

QY 12 VLAVLVAAAVTPATAQCQSQAGGAKCADCCLCCSQRFCTGTSYDYGPRCQSCCTCGG 71
Db 5 VLFVAVMAAA-TMAVABQCQSQAGGATPCNCLCCSRFGWGST-PYCGDQGCQSCQCG 62
QY 72 -----GGGVSASIVSRDLFERLLHRNDAAACLARGFYTYDAFLAAGAPPAFGTT 121
Db 63 GSTPVTTPSGGGVSSVSRALFDRMLLHRNDGACQAKGFYTYDAFVAASAFRGEGTT 122
QY 122 GDLTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEGSPSPSYCDQSDADWPCAP 181
Db 123 GGTDRKREVAAPFAQTSHTTGGWATAPDGAFAWGYCFKQEGATSNYCTTPSAQWPCAP 182
QY 182 GKQYGRGPIQLTHNYNGPAGRAIGVDLLNPNLVDATPTVAEFTAIWFMTTOSKNPS 241
Db 183 GKSYYGRGPIQLSHNYNGPAGRAIGVDLLNPNLVDATPTVSEKTAWMTAQAPKPS 242
QY 242 CHVITGLWPTARDASAGRPVPGVITNVINGIECGMGONDVADRIGFYKRYCPIFG 301
Db 243 SHAVITGQWSPGTDRAAGRPVPGVITNVINGIECGMGONDVADRIGFYKRYCPIFG 302
QY 302 IGYNNLDCYNQLSF 316
Db 303 VGYNNLDCYSQRPF 317

RESULT 2
CHI2_ORYSA
ID CHI2_ORYSA STANDARD; PRT; 336 AA.
AC P25765;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).
GN KCH10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91238706; PubMed=2034221;
RA Zhu Q., Lamb C.J.;
RT "Isolation and characterization of a rice gene encoding a basic
chitinase.";
RL Mol. Gen. Genet. 226:289-296(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
CC PIR; S15997; S15997.
CC HSSP; P23951; 2BAA.

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DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRIN3; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00026; CHITIN-BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 336 BASIC ENDOCHITINASE 2.
FT DOMAIN 22 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 24 39 BY SIMILARITY.
FT DISULFID 33 45 BY SIMILARITY.
FT DISULFID 38 52 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 336 AA; 35565 MW; 7F4EC126265DEA84 CRC64;

Query Match 68.6%; Score 1230; DB 1; Length 336;
Best Local Similarity 69.3%; Pred. No. 4.4e-87;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

QY 4 LRACAUAVLAVLVAAAVTPATAQCQSQAGGAKCADCCLCCSQRFCTGTSYDYGPRCQ 63
Db 1 MRALAVAMVAPPLAAAV---HAQCQSQAGGAVCNCLCCSQFGWGSTSDYCGAGCQ 57
QY 64 SQCT-----GCGGGGGVASTVSRDLFERLLHRNDAAACLARGFYTYDAFLAAGAF 115
Db 58 SOCSRLRRRPDASGGGSGVASTVSRSLFDLMLHRNDAAACPASNEYTYDAFAVAASAF 117
QY 116 PAFGTTGDLTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEG-GSPSYCDQS 174
Db 118 PGFAAGADATNKRKREVAALACTSHETGGWATAPDGPFTWGYCFKEENGAGDPDYCOQS 177
QY 175 ADWPCAPKQYVGRGPIQLTHNYNGPAGRAIGVDLLNPNLVDATPTVAEFTAIWFMT 234
Db 178 AQWPCAACKYVGRGPIQLSYNFYNGPAGQAIGADLLGDPDLVDASDATSFDTAFWFWMT 237
QY 235 TQSNKPSCHDVITGLWPTARDASAGRPVPGVITNVINGIECGMGONDVADRIGFYK 294
Db 238 PQSPKPSCNNAVATGQWTPSADDDQAGRVPVGYVITNVINGIECGHGHGDDRIADRIGFYK 297
QY 295 RYCDIFGIGYGNLDCYNO 313
Db 298 RYCDILGVSYGANLDCYSQ 316

RESULT 3
CHI1_ORYSA
ID CHI1_ORYSA STANDARD; PRT; 318 AA.
AC P24626;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV, JAPONICA; TISSUE=Seedling;
RA MEDLINE=91370899; PubMed=1993114;
RA Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
RA Muthukrishnan S., Reeck G.R.;
RT "Nucleotide sequence of a rice genomic clone that encodes a class I
endochitinase.";

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Query Match 66.8%; Score 1196.5; DB 1; Length 324;
Best Local Similarity 65.8%; Pred. No. 1.5e-84;
Matches 211; Conservative 42; Mismatches 58; Indels 9; Gaps 3;

QY 1 MSLRLARCATAVLAVYLAANAATPATAEQSGAGKACDCLCCSQFGTSDYCGP 60
DB 1 MSLRL-----IPILLVLVIFSCCSAQCGTQAGALCPGGLCCSKFGWCGSTSEYCGD 53

QY 61 RQSQCTGCGGGGGVYASIVSRDLPRFLLHRNDACIARGFTYDAFLAAGAFPAFT 120
DB 54 GCQSCSG-SSGGGTLSLISGDTFNMLKLRNDACQKPFYTYDAFLAAGAFPAFT 112

QY 121 TGLDTRKRREVAFFGQSHETTGWPTAPDGFPSGVCYKQSGPPSYCDOSADWPCA 180
DB 113 KGTATKKEIAFLAQTSHTTGGTAPDGPYANGYCFELRQ-NPSYQASSEFPFCA 171

QY 181 PGQYVGRPIQLTHNYNYGPAGRA.GVLLNNPDLVATDPTVAFKTAIWFMTQSNKP 240
DB 172 SGQYVGRPIQISWNYNYGQCRAIGVLLNNPDLVATDPTVAFKTAIWFMTQSNKP 231

QY 241 SCHDVTGLWTPATARSAGRVPGYVITNVINGTECGMGQNDKYADRIKRYCDIF 300
DB 232 SCHDVTGLWTPATARSAGRVPGYVITNVINGTECGMGQNDKYADRIKRYCDIF 291

QY 301 GIGYGNLDCYNOLSNFVGL 320
DB 292 GIGYGNLDCYSQRPFGSSL 311

RESULT 5
CHIL_SOLU STANDARD; PRT; 318 AA.
ID CHIL_SOLU STANDARD; PRT; 318 AA.
AC P52403;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTBL.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDES A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
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CC EMBL; U02605; AA18332.1; -.
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000509; Chitin_binding; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT NON_TER 1
FT SIGNAL <1 18
FT CHAIN 19 311
FT PROPEP 312 318
FT DOMAIN 19 60
FT DISULFID 21 36
FT DISULFID 30 42
FT DISULFID 35 49
FT DISULFID 54 58
FT SEQUENCE 318 AA; 33813 MW; A0B49DA528706AAA CRC64;
SQ
Query Match 66.6%; Score 1193; DB 1; Length 318;
Best Local Similarity 66.8%; Pred. No. 2.8e-84;
Matches 205; Conservative 42; Mismatches 58; Indels 2; Gaps 2;

QY 16 VLAAAAVTPATAEQSGAGKACDCLCCSQFGTSDYCGP-RCQSQCTGCGGGG 74
DB 7 LIFSULLLSASAEQSGAGKACDCLCCSKFGWCGDINDYCGNCSQCPGGPGSG 66

QY 75 GVASIVSRDLFERFLHRNDACIARG-FYTYDAFLAAGAFPAFTGDLTRKREVA 133
DB 67 DIGGVLSNMFQDLNHRNDACQGNFYNAFISAGSPFGTGTGDTARKREIAA 126

QY 134 FFGQTSHTTGGWPTAPDGFPSGVCYKQSGPPSYCDOSADWPCAPGKYVGRPIQL 193
DB 127 FFAQTSHTTGGWPTAPDGPYANGYCFELRQSGPQDYCTPSSQWPCAPGKRYVGRPIQI 186

QY 194 THNYNYGPAGRAIGVLLNNPDLVATDPTVAFKTAIWFMTQSNKPSCHDVITGLWTP 253
DB 187 SHNYNYGPCRAIGVLLNNPDLVATDSVLSFSAIWFMTQSNKPSCHDVITGRWQS 246

QY 254 ARDSAGRVPGYVITNVINGTECGMGQNDKYADRIKRYCDIFGIGYGNLDCYNQ 313
DB 247 GVDQAANRVPGYVITNVINGTECGMGQNDKYADRIKRYCDIFGIGYGNLDCGNQ 306

QY 314 LSFNVL 320
DB 307 RSPGNL 313

RESULT 6
CHIL_LYCES STANDARD; PRT; 322 AA.
ID CHIL_LYCES STANDARD; PRT; 322 AA.
AC Q05538;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE BASIC 30 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CHI9.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
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or send an email to license@isb-sib.ch).
-----
EMBL: X51599; CAA35945.1; -
EMBL: X64519; CAA45822.1; -
EMBL: M15173; RAA34070.1; -
PIR: A29074; A29074.
PIR: S13322; S13322.
PIR: S20981; S20981.
HSP: P23951; 2BA.
InterPro: IPR001002; Chitin_bind.
InterPro: IPR000726; glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; glyco_hydro_19; 1.
PRINTS: PR00451; CHITINBINDNG.
ProDom: PD000574; Glyco_hydro_19; 1.
ProDom: PD000609; Chitin_bind; 1.
SMART: SM00270; ChtBD1; 1.
PROSITE: PS00026; CHITIN_BINDING; 1.
PROSITE: PS00773; CHITINASE_19; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
Hydroxylation; Multigene family.
KW
FT SIGNAL 1 23
FT CHAIN 24 317 ENDOCHITINASE B.
FT PROPEP 318 324 REMOVED IN MAURE FORM (PROBABLE).
FT DOMAIN 24 65 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION.
FT MOD_RES 69 69 HYDROXYLATION.
FT SEQUENCE 324 AA; 34721 MW; FA65DC2113B3EB6 CRC64;

Query Match 56.1%; Score 1184; DB 1; Length 324;
Best Local Similarity 64.7%; Pred. No. 1.4e-83;
Matches 207; Conservative 46; Mismatches 63; Indels 4; Gaps 3;

QY 4 LRARCATAVLAVLAAAVTATAECQSQAGGAKACDCLCCSQFGCGTSDYCGP-RC 62
Db :| | | | :| | | | | | | | | | | | | | | | | | | | | |
1 MLRLREFTA-LSSLFSLLLSASAEQCGSQAGGARCASGLCCSKFGWGNNDYCGPGNC 59
QY 63 QSCCTG--CGGGGGVAVISVROLFERLLHRNDAACLAGFYDYDAFAAAGAPFAGT 120
Db :| | | | | | | | | | | | | | | | | | | | | | | | | | |
60 QSCQCPGPTFPGGDGLGSISSMFDQMLKHRNDNACQGGKFGVSYNAFINAARSFPFGGT 119
QY 121 TGLDLTRKREVAFAFGTSHETTGWPTAPDGPFSWGYCFKQCGSPSYCDQSDAWPCA 180
Db :| | | | | | | | | | | | | | | | | | | | | | | | | | |
120 SGTATARKREIAFAAFAQTSHETTGWATPDGPYAWGYCWLREGQSGDYCTPSGQWPCA 179
QY 181 PGKYYGGRGPIQLTHNYPAGRAIGVDLLNPNLDVATPTVAFKTAIWFWMTQSNKP 240
Db :| | | | | | | | | | | | | | | | | | | | | | | | | | |
180 PGRKYFGRGPIQISHNYPGCRRAIGVDLLNPNLDVATPDVTSFKALFWMTTPQSPKP 239
QY 241 SCHDVITGLWTPARDASAGRVGYVITNVINGIECGQNDKVDADRIGFYKRYCIDF 300
Db :| | | | | | | | | | | | | | | | | | | | | | | | | | |
240 SCHDVITGLWTPARDASAGRVGYVITNVINGIECGQNDKVDADRIGFYKRYCIDF 300
QY 301 GYGNNLDYNNQLSFNVL 320
Db :| | | | | | | | | | | | | | | | | | | | | | | | | | |
300 GVSFGDNLCCNQRFSTGNL 319

RESULT 8
Chit_TOBAC

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ID AC P08252; STANDARD; PRT; 329 AA.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
GN CHN48.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=CV HAVANA 425; TISSUE=Leaf;
EX MEDLINE=91346623; PubMed=1966383;
RA Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr.;
RT "Structure of a tobacco endochitinase gene: evidence that different
RT chitinase genes can arise by transposition of sequences encoding a
RT cysteine-rich domain.";
RL Plant Mol. Biol. 14:357-368(1990).
RN [2]
RP SUBCELLULAR LOCATION.
RX MEDLINE=92052270; PubMed=1946457;
RA Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
RT "A short C-terminal sequence is necessary and sufficient for the
RT targeting of chitinases to the plant vacuole.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
RN [3]
RP HYDROXYLATION.
RX MEDLINE=92358209; PubMed=1496378;
RA Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.;
RT "Vacuolar chitinases of tobacco: a new class of hydroxyproline-
RT containing proteins.";
RL Science 257:655-657(1992).
CC -|- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC -|- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -|- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -|- INDUCTION: BY ETHYLENE.
CC -|- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDES A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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EMBL: X16938; CAA34812.1; -
EMBL: X16939; CAA34813.1; -
PIR: S08627; S08627.
HSP: P23951; 2BA.
InterPro: IPR001002; Chitin_bind.
InterPro: IPR000726; glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; glyco_hydro_19; 1.
PRINTS: PR00451; CHITINBINDNG.
ProDom: PD000574; Glyco_hydro_19; 1.
ProDom: PD000609; Chitin_bind; 1.
SMART: SM00270; ChtBD1; 1.
PROSITE: PS00026; CHITIN_BINDING; 1.
PROSITE: PS00773; CHITINASE_19; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
Hydroxylation; Multigene family.
KW
FT SIGNAL 1 23
FT CHAIN 24 322 ENDOCHITINASE A.

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FT PROPEP 323 329 REMOVED IN MATURE FORM.
FT DOMAIN 24 55 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION (PARTIAL).
FT MOD_RES 69 69 HYDROXYLATION.
FT MOD_RES 71 71 HYDROXYLATION.
FT MOD_RES 72 72 HYDROXYLATION.
FT MOD_RES 74 74 HYDROXYLATION.
FT MOD_RES 75 75 HYDROXYLATION (PARTIAL).
SEQUENCE 329 AA; 35156 MW; 3EC99D96E6C0114C CRC64;

Query Match 65.9%; Score 1181; DB 1; Length 329;
Best Local Similarity 63.6%; Pred. No. 2.4e-83;
Matches 204; Conservative 44; Mismatches 65; Indels 8; Gaps 2;

QY 8 CATVALVLAARAAVTPATAECCGSGAGAKACDCLCCSQFGCGTTSYCGP-RQSQQC 66
DB 4 CFTALSSLLFSLLSASAECGSGAGARCPGLCCSKFGWCGNTNDYCGPGNCQSQC 63
QY 67 TG-----CGGGGGVASTVSRLPERLLHENDACIARGTYTYDAFLAAGATPAFG 119
DB 64 PGGPTPTPTPPGGGDLGSLISSMEDQMLKRNDCQCGKGYSTNAFTNAARSPFGFG 123
QY 120 TGGDLTRKREVAAPFGQTSHTTGWPTAPDGFPSWGYCFKQEGSPSPSCQSDADWPC 179
DB 124 TSGDTTARKRETAARFAAQTSHTTGWATAPDGPYANGYCWLRQEGSPGDTCTPSQWPC 183
QY 180 APCKQYRGPTQLTNNYNGPAGRAIGVDLLNPNPLVATDTPVAKTAIWFMTTQSNK 239
DB 184 APERKYFGRPQIISHNYNGCPGRAIGVDLLNPNPLVATDTPVISEKSAIWFMTTQSPK 243
QY 240 PSCHDVTITGLWPTARDSAAGRVPGYGVITNVLNGIEGGMQNDKVAADRIGYKYCDI 299
DB 244 PSCHDVIIGRWQPSAGDRAANRUPGVITNVLNGIEGGRGDSRVQDRIGFYRYSI 303
QY 300 FGIGYGNLDCYNQLSFNVLG 320
DB 304 LGVSPGDNLDGNGRSGFNGL 324

RESULT 9
CHI3_SOLITU STANDARD; PRT; 318 AA.
AC P52405;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTB3.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCRL_raxid-4u113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerthues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
RT and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
CC SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
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CC SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
CC OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U02607; AAA17409.1; --
CC HSSP; P23951; 2BAA.
CC InterPro; IPR001002; Chitin_bind.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00187; chitin_binding; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC ProDom; PD000609; Chitin_bind; 1.
CC SMART; SM00270; ChtBD1; 1.
CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
CC Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
CC Multigene family.
FT NON_TER 1 1 POTENTIAL.
FT SIGNAL <1 18 ENDOCHITINASE 3.
FT CHAIN 19 311 REMOVED IN MATURE FORM, VACUOLAR
FT PROPEP 312 318 TARGETING (POTENTIAL).
FT DOMAIN 19 60 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 21 36 BY SIMILARITY.
FT DISULFID 30 42 BY SIMILARITY.
FT DISULFID 35 49 BY SIMILARITY.
FT DISULFID 54 58 BY SIMILARITY.
FT SEQUENCE 318 AA; 33798 MW; BF587A9515534E71 CRC64;

Query Match 65.7%; Score 1177; DB 1; Length 318;
Best Local Similarity 67.4%; Pred. No. 4.7e-83;
Matches 201; Conservative 40; Mismatches 55; Indels 2; Gaps 2;

QY 25 ATAEQCGSQAGAKACDCLCCSQFGCGTTSYCGP-RQSQCTGCGGGGGVSVSRD 83
DB 16 ASAEQCGSQAGGALCAPGLCCSKFGWCGNTNDYCGPGNCQSQCPGGPSPGDIIGVINS 75
QY 84 LFERFLHNRNDAACLAR-GFYTYDAFLAAGAPPAFGTTGDLTRKREVAAPFGQTSHT 142
DB 76 MFDQMLNHRNDRNACQGNFYSNAFISAGSPFGTGTGTARRETAANFLAQTSHET 135
QY 143 TGGWPTAPDGPFTSWGYCFKQEGSPSPSCYCDQSDADWPCAPCKQYRGPIQLTHNYNGFA 202
DB 136 TGGWPSAPDGPYANGYCFELREQSGPGDYCTPSSQWPCAPGRKYFGRPQIISHNYNGPC 195
QY 203 GRAIGVDILNPNPLVATDTPVAKTAIWFMTTQSNKPSCHDVITGLWPTARDSAAGRV 262
DB 196 GRAIGVDLLNPNPLVATDSVISFKSAIWFMTTQSPKPSCHDVITGRWQPSGADQANRV 255
QY 263 PGYGVITNVLNGIEGGMQNDKVAADRIGYKYRCDIFGIGYGNLDCYNQLSFNVLG 320
DB 256 PFGVITNVLNGIEGCHGSDRSRVQDRIGFYRYCGILGVSPGDNLDGNGRSGFNGL 313

RESULT 10
CHI2_SOLITU STANDARD; PRT; 316 AA.
ID CHI2_SOLITU
AC P52404;
DT 01-OCT-1996 (Rel. 34, Created)
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DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
FT SIGNAL 1
FT CHAIN 21
FT DOMAIN 22 321
FT DOMAIN 22 62
FT DOMAIN 63 98
FT DOMAIN 99 321
FT DISULFID 24 39
FT DISULFID 33 45
FT DISULFID 38 52
FT DISULFID 58 62
SQ SEQUENCE 321 AA; 34847 MW; E87DBEBC8D7A2ADB CRC64;

Query Match 65.1%; Score 1166; DB 1; Length 321;
Best Local Similarity 69.1%; Pred. No. 3.2e-82;
Matches 206; Conservative 33; Mismatches 53; Indels 6; Gaps 4;

QY 26 TAEQCGSQAGGAKACDCLCCSQFGCGTTSYCGPR--CQSQCTGCGGGGVSIVSRD 83
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 SAEQCGRQAGALCPGLCCSQFGCGGNDYCKKENGCCQSCGSGDGTGLDLSLTRE 79
QY 84 LFERELHRNDACLARGFYTYDAFLAAGAPFAFGTGLDTRKREVAFAFGTSHETT 143
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 RFDQMLHRNDGGCPARGFYTYDAFLAAGAPFAFGTGLDTRKREVAFAFGTSHETT 139
QY 144 G--GWPTAPDGPFSWGYCFKQEGSQSPSYCDQADWPCAPGKQYIGRPIOLTHYNGP 201
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 GGAGW--AAPDGPYTWGYCYNREL--NPADYCOMDPNYPCAPGKQYEGRGMQLTWNYGQ 197
QY 202 AGRAIGVDLLNNPDVATPTVAFTAIWMTQSNKPSCHDVTITGLWPTARDSAGR 261
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
198 CGRAIGVDLLNNPDLLATPTISFKSAFWMTQSPKPSCHDVTITGLWPTARDSAGR 257
QY 262 VPGVGVTNVIINGIECGMGQNDKVADRIGFYKRYCDIFGIGYNNQLSFFNVG 319
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 VPGFGLTNIINGLEGCGGQGNARVEDRIGFYKRYCDITLGVGYNLLDYNQSYNNG 315

RESULT 12
CHIL_GOSHI
ID CHIL_GOSHI STANDARD; PRT; 324 AA.
AC Q39799;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Gossypium.
NCBI_TaxID=3635;
[1]
SEQUENCE FROM N.A.
RC STRAIN=CV; COKER 201;
RA Reverson J.F.; Chlan C.A.;
RT "Isolation of a genomic DNA clone from Gossypium hirsutum with high
RL similarity to class I endochitinase plant sequences.";
RL (In) Plant Gene Register PGR96-054.
CC -!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U60197; AAB67842.1; -.
CC HSSP; P02877; IHEV.
CC InterPro; IPR001002; Chitin_bind.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00187; chitin_binding; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC PRINTS; PR00451; CHITINBINDING.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC ProDom; PD000609; Chitin_bind; 1.
CC SMART; SM00270; ChtBD1; 1.
CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1
FT CHAIN 23
FT PROPEP 318 324
FT DOMAIN 23 64
FT DISULFID 25 40
FT DISULFID 34 46
FT DISULFID 39 53
FT DISULFID 58 62
SQ SEQUENCE 324 AA; 34666 MW; 9923B123EF5C7E3E CRC64;

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Query Match 64.9%; Score 1163; DB 1; Length 324;
Best Local Similarity 65.5%; Pred. No. 5.5e-82;
Matches 207; Conservative 41; Mismatches 62; Indels 6; Gaps 4;

QY 11 AVLAVLAAAAVTATATACGSGAGGAKACDCLCCSQFGCGTTSYCG--PRCSQCTGC 69
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6 ALSTFLLLLLVVVGSABEQCRQAGGALCPGLCCSQFGCGSTADYCTVPGCSQCSGS 65
QY 70 G--CGGGVASIVSRDLFERFLHRNDACLARGFYTYDAFLAAGAPFAFGTGLDTR 127
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 GPAPGPGGLTNLSRETFNQMLLHRNDGACPARGFYTYDAFLAARSPFAFTTGDQATR 125
QY 128 KREVAFAFGTSHETT--GWPTAPDGPFSWGYCFKQEGSQSPSYCDQADWPCAPGKQY 185
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 KREIAFAFIAQTSHETTGGAGW--AAPDGPYAWGYCYNRELNPSPSYCASDPNYPGKQY 184
QY 186 YGRGPIQLTHYNGYPAGRAIGVDLLNNPDVATPTVAFTAIWMTQSNKPSCHDV 245
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 FGRGPMLSWNYNGCGRAIGVDLLNNPDLLSDPTISFKSAFWMTQSPKPSCHNV 244
QY 246 ITGLWPTARDSAGRVPYGVYGVITNVIINGIECGMGQNDKVADRIGFYKRYCDIFGIGY 305
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 IIGAWSPSSSDRAAGRPVGYGVITNVIINGLEGCGGNAQVEDRIGFYKRYCDILGYSYG 304
QY 306 NLLDCYNQLSFFNVGLA 321
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
305 NLLDCYNQSPFGNGVS 320

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RESULT 13
CHIT_ARATH
ID CHIT_ARATH STANDARD; PRT; 322 AA.
AC P19171;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN MQC3.32
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;

```

```

RN  SEQUENCE FROM N.A.
RC  STRAIN-CV. COLOMBIA;
RA  Kaneko D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
RT  "Isolation and characterization of the genes encoding basic and
RL  acidic chitinase in Arabidopsis thaliana.";
RN  Plant Physiol. 93:907-914(1990).
[2]
RN  SEQUENCE FROM N.A.
RC  STRAIN-CV. COLOMBIA;
RX  MEDLINE=20363099; PubMed=10907853;
RA  Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
RT  "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RN  Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
RL  DNA Res. 7:217-221(2000).
CC  -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC  CONTAINING FUNGAL PATHOGENS.
CC  -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC  N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC  -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC  -!- TISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL IN ROOTS WITH LOWER
CC  LEVELS IN LEAVES AND FLOWERING SHOOTS.
CC  -!- INDUCTION: ETHYLENE INDUCES HIGH LEVELS OF SYSTEMIC EXPRESSION
CC  OF BASIC CHITINASE WITH EXPRESSION INCREASING WITH PLANT AGE.
CC  -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC  CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC  CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC  HYDROLASES).
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-----
ENBL; M38240; AAA32769.1; ALT_INIT.
DR  EMBL; AP002047; BAB03157.1; -.
DR  HSSP; P23951; 2BAA.
DR  InterPro; IPR001002; Chitin_bind.
DR  Pfam; PF00187; chitin_binding_1.
DR  Pfam; PF00182; Glyco_hydro_19; 1.
DR  PRINTS; PR00451; CHITINBINDING.
DR  ProDom; PD000574; Glyco_hydro_19; 1.
DR  ProDom; PD000609; Chitin_bind; 1.
DR  SMART; SM00270; ChtBD1; 1.
DR  PROSITE; PS00026; CHITIN_BINDING; 1.
DR  PROSITE; PS00773; CHITINASE_19.1; 1.
DR  PROSITE; PS00774; CHITINASE_19.2; 1.
KW  Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 315
FT  DOMAIN 21 63
FT  DISULFID 23 38
FT  DISULFID 32 44
FT  DISULFID 37 51
FT  DISULFID 56 60
SQ  SEQUENCE 322 AA; 34609 MW; C9AF6E4C544FCCD7 CRC64;

Query Match
Best Local Similarity 64.48; Score 1154; DB 1; Length 322;
Matches 206; Conservative 34; Mismatches 69; Indels 4; Gaps 2;

QY 10 TAVLAVLAAAVTAAEQCGSAGGACADCLCSQFQCTTSDYC-GPRCQSCQTC 68
Db 3 TNLFLFLSLLLSAQCQGRAGALCPNGLCSEFGWCGNTEPYCKQPCQSCQCTP 62
QY 69 CG---GGGGVASIVSKDLFERLLHRNDAACLAIRGFYTYDAFLAAAGAPPAFGTTGDL 125

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Db 63 GGPFPPTGDLSSQFDDMLKHRNDAAACPARGFYTYNAFITAAKSPFGFTGDTA 122
QY 126 TRKREVAFAFGQTSHETTGWPTAPDGPFSWGYCFKQEGSPSPYCDQADNPAPGKQY 185
Db 123 TRKKEVAFAFGQTSHETTGWATAPDGPYSGWGYCFKQEQNPASDYCEPSATWPCASGKY 182
QY 186 YGRGPITQLTHNYNGPAGRAIGVDLLNPDLYATDPTVAFKTAIWFMTQSNKPSCHDV 245
Db 183 YGRGPMQLSWNYNGLCGRGAIQVDLLNPDLYANDAVIAFAKAIWMTAQPKPSCHAV 242
QY 246 ITGLWPTARDASAAGRVPGYGVITVINGIECGMGQNDKVADRIGFYKRYCDIFGIGVG 305
Db 243 IAGQWQPSADRAAGRLPGYGVITNLINGLECGRQDGRVADRIGFYQRYCNIFGVNPG 302
QY 305 NMLDCYNQLSFNVGL 320
Db 303 GNLDYINQSRFVYNGL 317

RESULT 14
CH12_BRANA STANDARD; PRT; 322 AA.
ID CH12_BRANA
AC Q09023;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94143492; PubMed=8310072;
RA Hamel F., Bellemare G.;
RT "Nucleotide sequence of a Brassica napus endochitinase gene.";
RL Plant Physiol. 101:1403-1403(1993).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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ENBL; M95835; AAA32986.1; -.
DR  HSSP; P23951; 2BAA.
DR  InterPro; IPR001002; Chitin_bind.
DR  InterPro; IPR000726; Glyco_hydro_19.
DR  Pfam; PF00187; chitin_binding_1.
DR  Pfam; PF00182; Glyco_hydro_19; 1.
DR  PRINTS; PR00451; CHITINBINDING.
DR  ProDom; PD000574; Glyco_hydro_19; 1.
DR  ProDom; PD000609; Chitin_bind; 1.
DR  SMART; SM00270; ChtBD1; 1.
DR  PROSITE; PS00026; CHITIN_BINDING; 1.
DR  PROSITE; PS00773; CHITINASE_19.1; 1.
DR  PROSITE; PS00774; CHITINASE_19.2; 1.
KW  Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT  SIGNAL 1 20
FT  CHAIN 21 322
FT  DOMAIN 21 62
FT  DISULFID 23 38

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FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 322 AA; 34816 MW; E62BE4B17211DBCD CRC64;

Query Match
Best Local Similarity 64.0%; Score 1146; DB 1; Length 322;
Matches 205; Conservative 34; Mismatches 68; Indels 2; Gaps 2;

QY 10 TAVLVVLAATAVPTATAECGSGAGKACDCLCGSQGFCGTTSDYC-GPRCQSQCTG 68
Db 3 SCLELLIFSLFSFSLAECCGQAGALCPNGLCCSEFGWCGDTPAYCKQPCQSQCGG 62
QY 69 C-GGGGGVASIVSRDLERFLHRNDACLAGFYTYDAFLAAAGAFPAFTGDLDT 127
Db 63 TPFGPTGDLGSIISQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPGFTGTAT 122
QY 128 KREVAFFGQTSHETTGWPTADPGFSGYCFKQKQSGSPSYCDOSADWPAPGQYIG 187
Db 123 KKEIAFFGQTSHETTGWPTADPGFSGYCFKQKQSGSPSYCDOSADWPAPGQYIG 182
QY 188 RGPQLTHNNYAGPAGRAIGVLLNPNLDVATDPTVAFKTAIWFWMTQSNKPSCHDVIT 247
Db 183 RGPQLSWNNYQCGRAIGVLLNPNLDVATDPTVAFKTAIWFWMTQSNKPSCHDVIT 242
QY 248 GLWTPPTARDASAGRVPGYVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIYGN 307
Db 243 GOWQPSDADRAAGRVPGYVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIYGN 302
QY 308 LDCYNQLSF 316
Db 303 LDCYNQRSF 311
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RESULT 15
CHIX_PEA
ID CHIX_PEA STANDARD; PRT; 320 AA.
AC P36907;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV, BIRTE; TISSUE=Leaf;
RA Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
RA Collinge D.B.;
RT "Accumulation of defence-related transcripts and cloning of a
RT chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with
RT Ascochyta pisi lib.,"
RL Plant Sci. 92:69-79(1993).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- INDUCTION: BY FUNGAL INFECTION.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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```
CC or send an email to license@isb-sib.ch.
CC -----
DR EMBL; X63899; CAA45359.1; -
DR HSSP; P02877; 1HEV.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; CHUBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 320 ENDOCHITINASE.
FT DOMAIN 24 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 58 62 BY SIMILARITY.
SQ SEQUENCE 320 AA; 34507 MW; 7EDE8C81AECC3435 CRC64;

Query Match
Best Local Similarity 63.9%; Score 1145.5; DB 1; Length 320;
Matches 202; Conservative 32; Mismatches 55; Indels 9; Gaps 2;

QY 27 AEQCSQAGGAKCADCCLCGSQGFCGTTSDYCGPRCQSQCTGC-----GGGGGGVAS 78
Db 23 AEQCSQAGGAVCPNGLCCSKGFCGSTDYCGDGCQSQCKSPPTFTPTSGGSDVGR 82
QY 79 IYSRDLFERFLHRNDACLAGFYTYDAFLAAAGAFPAFTGDLDTKRREVAAPFGOT 138
Db 83 LVPSSLFQDLKRYRNDGRGAGHGFYTYDAFLAAARSFNGFTTGDNDTKKELAAFLAQT 142
QY 139 SHETTGGWPTADPGFSGYCFKQKQSGSPSYCDOSADWPCAPKQYGGPIQLTHNN 198
Db 143 SHETTGCWNTADPGFYANGYCFVSEQTQEVYCSPK-DWPCAPKKYIGRGPQLTHNN 201
QY 199 YGPAGRAIGVLLNPNLDVATDPTVAFKTAIWFWMTQSNKPSCHDVITGLWTPPTARDSA 258
Db 202 YGLAGQAIKEDLINPDLLSTNPTVSVFKTAIWFWMTPOANKPSHDVITGRWTPSAADSS 261
QY 259 AGRVPGYGVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIYGNLDCYNQLSF 316
Db 262 AGRVPGYGVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIYGNLDCYNQLSF 319
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Search completed: May 3, 2002, 18:48:32
Job time: 916 sec

1


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Db 61 CGGGTPTPTTPSGGGVSSVSRALEFDRMLLRNDGACQAKGFTYDAFAAAGAPP 120
QY 117 AFGTTGDLTRKREVAARFGQTSHTTGWPTAPDGPFFSWGYCFKQEQSPSPSCDSAD 176
Db 121 GFGTTGDTTRKREVAARFLAQTSHTTGWATAPDGAFAWGYCFKQEQGATSNICPSAQ 180
QY 177 WPCAGKQYGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAKTALWFWMTTQ 236
Db 181 WPCAPKSYGRGPIQLSHNYNGPAGRAIGVDLLNPNPLVATDPTVSKTAMFWMTAQ 240
QY 237 SNKPSCHVDITGLWPTARDASAGRVPGYGVITNVINGIEGGMQNDKQVADRIGFYKRY 296
Db 241 AKPSPSHAVITGQWSPSTDRAGRVPGYGVITNVINGIEGGMQNDKQVADRIGFYKRY 296
QY 297 CDIFGIGYGNLDYCNQLSF 316
Db 301 CDILRVGYGNLDYCNQRP 320

RESULT 2
Q43294 PRELIMINARY; PRT; 340 AA.
ID Q43294
AC Q43294
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
GN ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
OS Chial or Chp-2.
OC Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthoideae; Oryzoae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPONICA, CV. NIPPONBARE;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
RT of rice chitinase genes.";
RL Mol. Gen. Genet. 241:1-10(1993).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X56787; CA940107.1; -;
DR EMBL; D16222; BA03750.1; -;
DR HSSP; P23951; 2BAA.
DR Mendel; 727; Oryza; Chial; 727.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 340 CHITINASE.
SQ SEQUENCE 340 AA; 35586 MW; 642FE13928CA7BE CRC64;

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Query Match 74.0%; Score 1326.5; DB 10; Length 340;
Best Local Similarity 70.9%; Pred. No. 1.1e-111;
Matches 241; Conservative 29; Mismatches 53; Indels 17; Gaps 3;

QY 1 MSTLRACATA-----VLAVLAAAVTPATAEQCGSQAGKACADLCQSGFCGTTG 55
Db 1 MSTFRAAASLAKKAAVLAVLAAALATAARAEQCGAQAGKACPNCLCCSRWGCCTTS 60

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QY 56 DYCGPRCQSQCTGGC-----GGGGVASIVSRDLFFERLLHRNDAAACLAGFEYTYDA 107
Db 61 DFCGDCQSQCGCGGPTPTTPSPSDGVSIVPRDLFERLLHRNDGACPARGFYTYEA 120
QY 108 FLAAGAFAPAFGTGDLTRKREVAARFGQTSHTTGWPTAPDGPFFSWGYCFKQEQSP 167
Db 121 FLAAGAFAPAFGTGDLTRKREVAARFGQTSHTTGWPTAPDGPFFSWGYCFKQEQSP 180
QY 168 PSYQSDADWPCAPKQYGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAKT 227
Db 181 SDYQSPSEWPCAPKQYGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAKT 240
QY 228 ALWFMWTTQSNKPSCHVDITGLWPTARDASAGRVPGYGVITNVINGIEGGMQNDKVA 287
Db 241 ALWFMWTTQSNKPSCHVDITGLWPTARDASAGRVPGYGVITNVINGIEGGMQNDKVA 300
QY 288 DRIGFYKRYCDIFGIGYGNLDYCNQLSFN---VGLAAQ 323
Db 301 NRIGFYQRYCGAFGIGTGNLDYCNQRPFGSSVGLAEQ 340

RESULT 3
Q9SQL3 PRELIMINARY; PRT; 320 AA.
ID Q9SQL3
AC Q9SQL3
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CHITINASE.
GN Ch12.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poae; Poa.
OX NCBI_Taxid=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF000966; AAF04454.1; -;
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 320 AA; 33711 MW; BEFC3ADBEC39B5 CRC64;

Query Match 73.5%; Score 1317.5; DB 10; Length 320;
Best Local Similarity 72.6%; Pred. No. 6.7e-111;
Matches 228; Conservative 33; Mismatches 44; Indels 9; Gaps 1;

QY 12 VLAVLAAAVTPATAEQCGSQAGKACADLCQSGFCGTTGSDYCGPRCQSQCTGGG 71
Db 5 VVVTILVAFAVSAHAEEQCGSQAGGATCPNCLCCSKFGCGTTSYDYGTCGQCGQCNCSG 64
QY 72 -----GGGGVASIVSRDLFFERLLHRNDAAACLAGFEYTYDAFLAAAGAPAFGTG 122
Db 65 PTPVTPPSGGGGVSSIVSGLFEQMLLRNDAAACLAGFEYTYDAFLAAAGAPAFGTG 124
QY 123 DLDTTRKREVAARFGQTSHTTGWPTAPDGPFFSWGYCFKQEQSPSPSCDSADWFCAPG 182
Db 125 STDVRKREVAARFLAQTSHTTGWPTAPDGPFFSWGYCFKQEQGATSDYCSFSSQWFCAPG 184

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RC STRAIN-CV. HASS; TISSUE=MESOCARP;
RA Souka S., Hsieh L., Krebitz W., Akasawa A., Martin B., Starrett D.,
RA Peterbauer C., Scheiner O., Breiteneder H.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 278202; CAB01591.1; -.
DR HSSP; P02877; IHEV.
DR Mendel; 14766; Perae; Chial; 14766.
DR InterPro; IPR001002; Chitin_bind.
DR Pfam; PF00187; chitin_binding; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR Chitin-binding; Glycosidase; Hydrolase; Signal.
KW SIGNAL
FT CHAIN 26 326 ENDOCHITINASE.
FT SEQUENCE 325 AA; 34586 MW; 643B20589E062E61 CRC64;

Query Match 70.1%; Score 1256; DB 10; Length 326;
Best Local Similarity 69.8%; Pred. No. 2.4e-105;
Matches 220; Conservative 36; Mismatches 55; Indels 4; Gaps 2;

QY 12 VLAVVLAANAATPATAECGSGOAGGAKCADCCLCCSQFGCGTTSDYCGPCRCQSOCTG-CG 70
DB 10 LLLLLLVLLGAGFAECGQAGGALCPGLCCSQFGCGSTSDYCGPCRCQSOCTGVP 69
QY 71 GGGGVASIVSRDLFERFLHRNDACIARGFYTYDAFLAAAGAPPAFGTTGDLTRKRE 130
DB 70 SPGGGVASLISQSVENQMLKRNDAACQAKGYTYNAFLAAANSFNGFASVGDATARKRE 129
QY 131 VAAEFQGT-SHETGGWTPADPGPSWGYCFKQEGSPSCDQSDADWPCAPGKQYGRGP 190
DB 130 IAAFLNQISHETGGWATPDGPTAWGYCFKQEGNPFDPVCVTAQWPCAPGKQYGRGP 189
QY 191 IQLTHNYNGPAGRAIGVDLLNPDVATDPTVAFKTAIWFMTQSNKPSCHDVITGLW 250
DB 190 IQISYNYNGPAGRAIGVDLLNPDVATDPTVAFKTAIWFMTQSNKPSCHDVITGLW 249
QY 251 TPTARSDAAGRPVGYGVITNINGSIEGCGQNDKVADRIGFYKRYCDIFGIGYGNLDC 310
DB 250 TPTAARDRAAGRLPGYGVITNINGSIEGCGKFNDAVDRIGFYKRYCDIFGIGYGNLDC 309
QY 311 YNQLSFNVG---LAA 322
DB 310 YNORSFGVSTNPLAA 324

RESULT 11
Q9SOL4 PRELIMINARY; PRT; 340 AA.
AC Q9SOL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE CHITINASE.
GN CH11.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000964; AAF04453.1; -.

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DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR Pfam; PF00187; chitin_binding; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR Chitin-binding.
KW Chitin-binding.
FT CHAIN 340 AA; 36011 MW; 3613D7059A871E94 CRC64;

Query Match 70.0%; Score 1254; DB 10; Length 340;
Best Local Similarity 69.3%; Pred. No. 3.8e-105;
Matches 219; Conservative 40; Mismatches 45; Indels 12; Gaps 3;

QY 12 VLAVVLAANAATPATAECGSGOAGGAKCADCCLCCSQFGCGTTSDYCGPCRCQSOCTGCG 71
DB 6 VAILVAAFAVS-AHAECQCGSGAGGATCNCCLCKSKFGCGTTSDYCGTGCQSCNCGSG 64
QY 72 -----GGGVASIVSRDLFERFLHRNDACIARGFYTYDAFLAAAGAPPAFGTTG 122
DB 65 PTPVTPSPGGGVSSLVQSLEFQMLHRNDPSCQANGFYTKAFIAAANSFAGFGTTG 124
QY 123 DLTRKREVAAPFGQSHETGGWTPADPGPSWGYCFKQEGSPSCDQSDADWPCAPG 182
DB 125 STDVRRKREVAFAAQSHETGGWTPADPGPSWGYCFKQEGATSDYCSFSSOWPCAPG 184
QY 183 KQYGRGPIQLTHNYNGPAGRAIGVDLLNPDVATDPTVAFKTAIWFMTQSNKPS 242
DB 185 KKYEGGPIQISYNYNGPAGRAIQTDLLNPDVLSNATVSEFALFWMTAQSPKSS 244
QY 243 HDVITGLWTPARSDAAGRPVGYGVITNINGSIEGCGQNDK--VADRIGFYKRYCDIF 300
DB 245 HAVITGWSPPSSDAAGRPVGYGVITNINGSIEGCGQNDKRVAVADRIGFYKRYCDIL 304
QY 301 GIGYGNLDCYNLSF 316
DB 305 GVSYGDLDCYNESPF 320

RESULT 12
Q42993 PRELIMINARY; PRT; 323 AA.
AC Q42993;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-
DE POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CH1AL OR CHT-1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartolidae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
RT of rice chitinase genes."
RL Mol. Gen. Genet. 241:1-10(1993).
RN [2]
RP SEQUENCE OF 21-323 FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Nishizawa Y., Hibi T.;
RL Plant Sci. 76:211-218(1991).

```

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DB ENZY. C1000

CC	-1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC	ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR	EMBL; D16221; BAA33749.1; -
DR	EMBL; X56063; CAA39355.1; -
DR	HSP; P23951; 2BAA.
DR	Mengel; 14776; Orysa;Chial;14776.
DR	InterPro; IPR001002; ChitinBind.
DR	InterPro; IPR000726; Glyco_hydro_19.
DR	Pfam; PF00187; chitin_binding; 1.
DR	Pfam; PF00182; Glyco_hydro_19; 1.
DR	PRINTS; PR00451; CHITINBINDNG.
DR	ProDom; PD000574; Glyco_hydro_19; 1.
DR	ProDom; PD000609; ChitinBind; 1.
DR	SMART; SM00270; ChtBD1; 1.
DR	PROSITE; PS00773; CHITINASE_19.1; 1.
DR	PROSITE; PS00774; CHITINASE_19_2; 1.
DR	PROSITE; PS00026; CHITIN_BINDING; 1.
KW	Chitin-binding; Glycosidase; Hydrolase; Signal.
FT	FT SIGNAL 21 20
FT	CHAIN 21 323
FT	SEQUENCE 323 AA; 33764 MW; IC85B6227A33EE06 CRC64;
DR	ENDOCHITININASE.
DR	SEQUENCE 323 AA; 33764 MW; IC85B6227A33EE06 CRC64;

Query Match 69.1%; Score 1238.5; DB 10; Length 323;
Best Local Similarity 69.3%; Pred. No. 8.9e-104;
Matches 224; Conservative 31; Mismatches 51; Indels 17; Gaps 4;

[illegible]

```

RESULT 13
38777
D 038777 PRELIMINARY; PRT; 318 AA.
T C Q38777;
T 01-NOV-1996 (TREMBlrel. 01, Created)
T 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
T 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
E CHITINASE PRECURSOR (FRAGMENT).
E CHIAL OR CHITINASE.
S Allium sativum (Garlic).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
C Allium.
X NCBI_TaxID=4682;
X [1]
P SEQUENCE FROM N.A.
A Van Damme E.J., Willems P., Peumans W.;
A Submitted (MAY-1992) to the EMBL/Genbank/DBJ databases.
R EMBL; M94105; AAA32641.1; -.
R HSSP; P23951; 2BAA.
R Mendel; 705; Allsa:Chial.705.

```

DR		InterPro: IPR001002; Chitin_bind.	
DR	DR	InterPro: IPR000726; Glyco_hydro_19.	
DR	DR	Pfam: PF00187; chitin_binding; 1.	
DR	DR	Pfam: PF00182; Glyco_hydro_19; 1.	
DR	DR	PRINTS: PR00451; CHITINBINDNG.	
DR	DR	ProDom: PD000574; Glyco_hydro_19; 1.	
DR	DR	ProDom: PD000609; Chitin_bind; 1.	
DR	DR	SMART: SM00270; ChtBD1; 1.	
DR	DR	PROSITE: PS00773; CHITINASE_19_1; 1.	
DR	DR	PROSITE: PS00774; CHITINASE_19_2; 1.	
DR	DR	PROSITE: PS00026; CHITIN_BINDING; 1.	
KW		Chitin-binding; Signal.	
FT	NON_TER	1	
FT	SIGNAL	<1 17	POTENTIAL.
FT	CHAIN	18 318	CHITINASE.
SQ	SEQUENCE	318 AA; 33175 MW;	097C3DBD0772468D4 CR064;

Query Match 67.7%; Score 1213; DB 10; Length 318;
Best Local Similarity 66.9%; Pred. No. 1.7e-101;
Matches 212; Conservative 39; Mismatches 54; Indels 12. Cons 1.

[illegible]

```

RESULT 14
338776
D D Q38776 PRELIMINARY; PRT; 302 AA.
C C Q38776;
T T 01-NOV-1996 (TREMBLrel. 01, Created)
T T 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
T T 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
E E CHITINASE PRECURSOR (FRAGMENT).
E E CHIAL OR CHITINASE.
N N Allium sativum (Garlic).
S S Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
C C Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
C C Allium.
X X NCBI_TaxID=4682;
X X [1]
P P SEQUENCE FROM N.A.
L L Van Damme E.J., Willemis P., Peumans W.:
L L Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
R R EMBL; M94106; AAA32640.1; -.
R R HSS; P23951; 2BAA.
R R Mendel; 704; Allisa; Chial; 704.
R R InterPro; IP001002; Chitin_bind.
R R InterPro; IP000726; Glyco_hydro_19.
R R Pfam; PF00187; chitin_binding; 1.
R R Pfam; PF00182; Glyco_hydro_19; 1.
R R PRINTS; PR00451; CHITINBINDING.

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DR ProDom: PD000574; Glyco_hydro_19; 1.
 DR SMART: SM00270; Chitinase_19; 1.
 DR PROSITE: PS00773; CHITINASE_19.1; 1.
 DR PROSITE: PS00774; CHITINASE_19.2; 1.
 DR PROSITE: PS00026; CHITIN_BINDING; 1.
 KW Chitin-binding; Signal.
 FT NON_TER <1 17
 FT SIGNAL 18 302
 FT CHAIN 18 302
 FT CHITINASE.
 SQ SEQUENCE 302 AA; 31728 MW; D0687D330BFFD75F CRC64;

Query Match 67.2%; Score 1204; DB 10; Length 302;
 Best Local Similarity 69.4%; Pred. No. 1.1e-100;
 Matches 209; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

QY 16 VLAAAVTPATAVOCGSGAGGAKCADCCLCCSQFGCGTTSYDYGPRCQSCQCTCGCGGGGG 75
 DB 2 VITPALEFTNSYAQCGSGGALCSNGLCCSQYGYCGNGPGYCGTGCQSCGCGGGGGSG 61
 QY 76 VASIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAGAPPAFGTTGSLDTRKREVAAPF 135
 DB 62 VASIISSLEFNQMLHRNDAAACAPANGFYTIDAFIAAANSESGFTGTDITQKRELAAPF 121
 QY 136 GOTSHTTGGTPTADPGPSNGYCFKQSGPSYCDOSADWFCAPGKQYGRPIQLTH 195
 DB 122 AGTSHTTGGYASAPDGYAWGYCFKQSGNPPDYCQASQYPCAPGKQYGRPIQLSY 181
 QY 196 NYNYGPAGRAIGVDLNNPDLVATDPTVAFKTAIWFMNTTQSNKPSCHDVITGLWTPAR 255
 DB 182 NYNYGCGNAINQDLLNPNLDVADPAISPKTAIWFWNTAOSPKPSCHAVATGOWOPSAA 241
 QY 256 DSAAGRVPGYGVITNVINGTECGMGNDKVADRIQYKCYDIFGIGYGNLDCYNQLS 315
 DB 242 DDAAGRVFGYGVITNVINGTECGMGNDKVADRIQYKCYDIFGIGYGNLDCYNQLS 301
 QY 316 F 316
 DB 302 F 302

RESULT 15
 Q42995
 ID Q42995 PRELIMINARY; PRT; 322 AA.
 AC Q42995;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
 DE ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
 GN CHIA1 OR RC24.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IR36; TISSUE=LEAF;
 RX MEDLINE=96189256; PubMed=8605293;
 RA Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
 RT "Regulation, expression and function of a new basic chitinase gene in
 RT rice (Oryza sativa L.).";
 RL Plant Mol. Biol. 30:387-401(1996).
 CC -/- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
 CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
 DR ENMBL; X87109; CAA60590.1; -;
 DR RSP; P23951; 2BAA.
 DR Mendel; 1634; Oryza; Chial; 1634.
 DR InterPro; IPR001002; Chitin bind.
 DR InterPro; IPR000726; Glyco_hydro_19.
 DR Pfam; PF00187; chitin_binding; 1.
 DR Pfam; PF00182; Glyco_hydro_19; 1.

DR PRINTS; PR00451; CHITINBINDNG.
 DR ProDom: PD000574; Glyco_hydro_19; 1.
 DR ProDom: PD000609; Chitin_bind; 1.
 DR SMART: SM00270; Chitinase_19; 1.
 DR PROSITE: PS00773; CHITINASE_19.1; 1.
 DR PROSITE: PS00774; CHITINASE_19.2; 1.
 DR PROSITE: PS00026; CHITIN_BINDING; 1.
 KW Chitin-binding; Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 20
 FT SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;

Query Match 56.5%; Score 1192; DB 10; Length 322;
 Best Local Similarity 67.2%; Pred. No. 1.4e-99;
 Matches 217; Conservative 30; Mismatches 56; Indels 20; Gaps 5;

QY 9 ATAVLAVLAAAVTPATAVOCGSGAGGAKCADCCLCCSQFGCGTTSYDYGPRCQSCQCT- 67
 DB 5 ALVVATAFAVAVQP---EQCGSQARGALCPNCLCCSQYGCWGSTAYCGSGCQSCSR 61
 QY 68 -----GCGGGGGGVAIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAGAPPAF 118
 DB 62 QLRRRRPDRPSGGGGGVAIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAGAPPAF 121
 QY 119 GTTGDLTRKREVAAPFGOTSHETGGWPTADPGPSNGYCFKQSGPSYCDQS 174
 DB 122 ATTGDAATRKREVAAPLAQISHETMGWATADPGPSNGYCFKQSGPSYCDQS 179
 QY 175 ADWPCAPGKQYGRPIQLTHNYNYPAGRAIGVDLNNPDLVATDPTVAFKTAIWFMNT 234
 DB 180 SQMPCRAKGYGRPIQLTHNYNYPAGRAIGVDLNNPDLVATDPTVAFKTAIWFMNT 236
 QY 235 TQSNKPSCHDVITGLWTPARSAAGRVPGYGVITNVINGTECGMGNDKVADRIQYK 294
 DB 239 POSKPSCHAVMTGQWTPNCDQAGRVPGYGVITNVINGTECGMGNDKVADRIQYK 298
 QY 295 RYCDIFGIGYGNLDCYNQLSFN 317
 DB 299 RYCDMLGVSYGANLDCYNORPFN 321

Search completed: May 3, 2002, 18:47:01
 Job time: 885 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:30:30 ; Search time 117.39 Seconds
 (without alignments)
 201.290 Million cell updates/sec

Title: US-09-534-229c-3
 Perfect score: 1765
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_ll01.*

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 22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1765	100.0	319	22	AA1980
2	1688.5	95.7	318	20	AA198079
3	1597.5	90.5	298	20	AA198080
4	1301.5	73.7	336	13	AA199019
5	1301.5	73.3	336	16	AA199019
6	1294.5	73.3	323	22	AA198488
7	1291.5	73.2	326	22	AA198444
8	1270.5	72.0	329	12	AA195841
9	1256.5	71.2	331	12	AA191305
10	1252	70.9	324	12	AA193275
11	1252	70.9	324	18	AA193129

12	1252	70.9	324	21	AA197513	Amino acid sequenc
13	1202.5	68.1	328	13	AA192082	Sequence of endoch
14	1202.5	68.1	329	15	AA195860	Endochitinase pr
15	1192.5	67.6	317	17	AA1900186	American elm chiti
16	1156	65.5	292	18	AA1924554	Chitinase. Cucurb
17	1132.5	64.2	303	13	AA1920820	Sequence of a 302
18	1125	63.7	266	15	AA1952577	Chitinase G. Hord
19	1066	60.4	328	19	AA1964776	Floral organ-speci
20	1003	56.8	2466	20	AA1905844	Banana ripening fr
21	927	52.5	243	20	AA190169	C. ensiformis chit
22	805.5	45.6	254	12	AA1913274	Petunia extracellu
23	805.5	45.6	254	18	AA1931296	Petunia hybrida ex
24	805.5	45.6	254	21	AA1907512	Amino acid sequenc
25	804.5	45.6	284	21	AA1918905	A maize chitinase
26	794	45.0	439	13	AA1928150	Sugar beet chitina
27	786.5	44.6	272	21	AA1928415	Arabidopsis thalia
28	786.5	44.6	280	21	AA1928414	Arabidopsis thalia
29	777.5	44.1	253	16	AA1976714	Tobacco endochitin
30	777	44.0	259	21	AA1918902	A maize chitinase
31	769.5	43.6	252	21	AA1918903	A maize chitinase
32	757	42.9	252	20	AA1998081	Rye chitinase-like
33	756	42.8	230	20	AA1998082	Rye chitinase-like
34	734	41.6	256	22	AA1911487	Wheat chitinase pr
35	722.5	40.9	372	22	AA1928788	Protein encoded by
36	710.5	40.3	250	16	AA1976713	Wild tomato endoch
37	710.5	40.3	253	16	AA1976712	Wild tomato endoch
38	618	35.0	281	21	AA1918894	A maize chitinase
39	612.5	34.7	155	21	AA1918906	Amino acid sequenc
40	602	34.1	271	21	AA1918904	A maize chitinase
41	602	34.1	271	21	AA1918936	Amino acid sequenc
42	597.5	33.9	268	13	AA1928147	Sugar beet chitina
43	563	31.9	264	13	AA1928145	Sugar beet chitina
44	515.5	29.2	261	21	AA1918896	A maize chitinase
45	504.5	28.6	813	21	AA1953657	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AA1911489 standard; protein; 319 AA.
 XX AA1911489;
 AC AA1911489;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Wheat chitinase protein homologous to spring wheat chitinase.
 XX
 KW Wheat; chitinase; low temperature expression; hardened; plant;
 XX snow mould resistance; psychophilic plant pathogen; spring wheat.
 OS Triticum aestivum.
 XX
 PN JP2000270866-A.
 XX
 PD 03-OCT-2000.
 XX
 PF 25-MAR-1999; 99JP-0081694.
 XX
 PR 25-MAR-1999; 99JP-0081694.
 XX
 PA (HOKK-) HOKKAIDO NOGO SHIKENBACHO.
 XX
 DR WPI; 2001-027417/04.
 XX
 PT New low temperature expression chitinase gene for producing a plant
 XX grade highly resistant to psychophilic plant pathogenic microbes
 PS Claim 7; Fig 3; 11pp; Japanese.
 XX
 CC This invention describes novel wheat chitinase genes. The invention also
 CC describes a method for the isolation of a low temperature expression

CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat P1173438 (of high snow mould resistance). The genes are
 CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.
 CC
 XX Sequence 319 AA;

Query Match 100.0%; Score 1765; DB 22; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1.1e-137;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 DB 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 QY 61 GCSGGTVPVPTPSGGVSSIIQSFLDQMLLRNDAACIAKAGFYNGAFVAAANSFSGF 120
 DB 61 GCSGGTVPVPTPSGGVSSIIQSFLDQMLLRNDAACIAKAGFYNGAFVAAANSFSGF 120
 QY 121 ATGSTDVKKREVAFLAQTHSHETTGWPTAPDGPYSGWYCFNBERGATSDYCTPSSQWP 180
 DB 121 ATGSTDVKKREVAFLAQTHSHETTGWPTAPDGPYSGWYCFNBERGATSDYCTPSSQWP 180
 QY 181 CAPGKKYFGRGPIQISHNYNYPAGQAIGTDLNNPDIVASDATVSKTALWFWMTQSP 240
 DB 181 CAPGKKYFGRGPIQISHNYNYPAGQAIGTDLNNPDIVASDATVSKTALWFWMTQSP 240
 QY 241 KPSSHDTVITGRWSPSGADQAAGVPCYGVITNINGLGCGRGQDGRVADRIGFYKRYCD 300
 DB 241 KPSSHDTVITGRWSPSGADQAAGVPCYGVITNINGLGCGRGQDGRVADRIGFYKRYCD 300
 QY 301 LLGVSYGDNLDYCNQRPFA 319
 DB 301 LLGVSYGDNLDYCNQRPFA 319

RESULT 2
 AAW98079
 ID AAW98079 standard; Protein; 318 AA.
 XX
 AC AAW98079;
 DT 21-JUN-1999 (first entry)
 XX
 DE Rye chitinase-like protein CHT9 preproteins.
 XX
 KW CHT9; chitinase-like protein; antifreeze protein; AFP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.
 XX
 OS Secale cereale.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /note= "signal peptide"
 FT Protein 21..318
 FT Protein /note= "mature protein, also claimed in Claim 10"
 PN WO9906565-A2.
 XX
 XX 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-CA00745.
 XX
 PR 31-JUL-1997; 97US-0903872.
 XX
 PA (ICEB-) ICE BIOTECH INC.
 XX
 PI Griffith M, Hew C, Moffatt B, Xiong F;
 XX
 XX WPI: 1999-153795/13.
 DR N-FSDP; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -
 PT particularly with chitinase activity, used to impart frost, and
 PT pathogen, resistant to plants, for preservation of foods, cells etc.
 PT and for treating tumours
 XX
 XX Claim 10; Fig 21a; 118pp; English.

The present sequence is winter rye (Secale cereal L. cv. Muskateer) CHT9 preprotein. The mature protein, which is also claimed, is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT9 cDNA (see AAX24889) was obtained by isolating mRNA from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed. CHT9 and CHT46 (see AAW98081-82) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze proteins can be used: to increase the freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved biological material. The signal peptide can be used to direct protein secretion in transgenic organisms or expression systems.

SQ Sequence 318 AA;

Query Match 95.7%; Score 1688.5; DB 20; Length 318;
 Best Local Similarity 95.3%; Pred. No. 2.1e-131;
 Matches 304; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

QY 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 DB 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 QY 61 GCSGGTVPVPTPSGGVSSIIQSFLDQMLLRNDAACIAKAGFYNGAFVAAANSFSGF 120
 DB 61 GCSGGTVPVPTPSGGVSSIIQSFLDQMLLRNDAACIAKAGFYNGAFVAAANSFSGF 120
 QY 121 ATGSTDVKKREVAFLAQTHSHETTGWPTAPDGPYSGWYCFNBERGATSDYCTPSSQWP 180
 DB 121 ATGSTDVKKREVAFLAQTHSHETTGWPTAPDGPYSGWYCFNBERGATSDYCTPSSQWP 180
 QY 181 CAPGKKYFGRGPIQISHNYNYPAGQAIGTDLNNPDIVASDATVSKTALWFWMTQSP 240
 DB 181 CAPGKKYFGRGPIQISHNYNYPAGQAIGTDLNNPDIVASDATVSKTALWFWMTQSP 240
 QY 241 KPSSHDTVITGRWSPSGADQAAGVPCYGVITNINGLGCGRGQDGRVADRIGFYKRYCD 300
 DB 241 KPSSHDTVITGRWSPSGADQAAGVPCYGVITNINGLGCGRGQDGRVADRIGFYKRYCD 300
 QY 301 LLGVSYGDNLDYCNQRPFA 319
 DB 301 LLGVSYGDNLDYCNQRPFA 318

RESULT 3
 AAW98080
 ID AAW98080 standard; Protein; 298 AA.
 XX
 AC AAW98080;
 DT 21-JUN-1999 (first entry)
 XX
 DE Rye chitinase-like protein CHT9.
 XX
 KW CHT9; chitinase-like protein; antifreeze protein; AFP;

KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.
 XX
 OS Secale cereale.

XX WO9906565-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

XX (ICEB-) ICE BIOTECH INC.

XX Griffith M, Hew C, Moffatt B, Xiong F;

XX WPI; 1999-153795/13.

XX N-PSDB; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -
 PT particularly with chitinase activity, used to impart frost, and
 PT pathogen, resistant to plants, for preservation of foods, cells etc.
 PT and for treating tumours
 XX
 PS Claim 10; Fig 21d; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
 CC CHT9 mature protein. It lacks the 20-amino acid signal peptide
 CC of the preprotein (see AAW98079), which is also claimed. Mature CHT9
 CC is a chitinase-like protein that has chitinase (antifungal) and
 CC antifreeze activities. CHT9 preprotein cDNA (see AAX24889) was
 CC obtained by isolating mRNA from rye plants grown at low temperatures
 CC in the absence of pathogens or other stresses, i.e. under conditions
 CC when only chitinases with antifreeze activity would be expressed.
 CC CHT9 and CHT46 (see AAW98081-82) have been cloned and expressed in
 CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
 CC The chitinase-like antifreeze proteins can be used: to increase
 CC freezing tolerance of plants and microorganisms; to increase field
 CC survival of plants, animals and microorganisms exposed to sub-zero
 CC temperatures; to inhibit ice recrystallisation in biological
 CC materials or foods; for cryopreservation and hypothermic protection
 CC of cells, embryos, tissues etc. (particularly human platelets); and
 CC to kill tumour cells. They are also used to inhibit initiation and
 CC progression of diseases or spoilage caused by low temperature
 CC pathogens (particularly fungi) in plants, frozen foods and any
 CC cryopreserved biological material.

XX Sequence 298 AA;

Query Match 90.5%; Score 1597.5; DB 20; Length 298;
 Best Local Similarity 95.0%; Pred. No. 6.3e-124;
 Matches 284; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

QY 21 EQCGAGGATCPNCLCCSKFGCGTSDYCGTCGCGCQSCGCGTVPVPTPSGGVSS 80

DB 1 eqcgagggatcpnclccskrfgcgsteycgdcgqcnrc-99tvpvpptpgggvss 59

QY 81 IISQSLFDQMLLRNDAACLAKEFYNYGAFVAAANSFSGFATTGSTDYKKREVAFLAQT 140

DB 60 iisqslfdqmlrrndaacilaekfyngafiaaansfgfattgtdvrkrevaflaqt 119

QY 141 SHETTGMPAPDGPYSGWYCFNBERGATSDYCFPSOWCAPGKKYFGRPIQISHN 200

DB 120 shettgwtapdgpysgwycfngergapsdycpsqdwpcapgkkyfgrgpiqisyn 179

QY 201 YCPAQATGTLNPNPLVADATVFKTALWMTPOSBPSSHDVITGWSPSGADQA 260

DB 180 ycpagraigtldlnmpdlvadatvfktafwmtposbpsshdvltgrwpsgagda 239

QY 261 AGRVPGYGVITNIINGLECGRGQDGRVADRIGFYKRYCDLIGVSYGDNLCYNORPFA 319

|||||

DB 240 agrvpgygvitniinglecgrgqdarvadrigfykrycdllgsvygdnlcdynqrfa 298

RESULT 4

AAR29019

ID AAR29019 standard; Protein; 336 AA.

XX AAR29019;

XX 20-APR-1993 (first entry)

XX RCH10 chitinase protein.

XX Promoter; region; rice; chitinase; physical; biological; stress;

KW leaves; stems; roots; male; female; reporter; monocotyledon;

KW dicotyledon; development; plant; defence; selectable; genes.

XX Oryza sativa.

XX Key Location/Qualifiers

FT Region 123..323

FT /note= "Region conserved between class I and class

FT II chitinases"

XX WO9220807-A.

XX 26-NOV-1992.

XX 21-MAY-1992; 92WO-US04282.

XX 22-MAY-1991; 91US-0704288.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Lamb CJ, Zhu Q;

XX WPI; 1992-415785/50.

XX N-PSDB; AAQ31407.

XX DNA fragment contg. chitinase gene and its regulatory region - is

XX responsive to mature plant stress and has low level expression in

XX leaves, moderate level expression in stem and high level

XX expression in roots

XX Disclosure; Page 33-34; 45pp; English.

XX The sequence given is encoded by the rice chitinase gene. The promoter

XX region of this gene (see AAQ31407) is responsive to physical and/or

XX biological stress. The pattern of expression of this protein in mature

XX plants is characteristic. There is a low level of expression in

XX leaves, a moderate level in plant stems and the highest level in roots

XX and the male and female parts of the plant. The chitinase promoter

XX sequence may be linked to a reporter gene for expression in mono- or

XX dicotyledon plants. Expression of this reporter gene may be used to

XX study patterns of development and controlled expression of plant

XX defence genes and selectable genes.

XX Sequence 336 AA;

Query Match 73.7%; Score 1301.5; DB 13; Length 336;
 Best Local Similarity 72.3%; Pred. No. 1.8e-99;
 Matches 237; Conservative 27; Mismatches 47; Indels 17; Gaps 4;

QY 1 MRGVVVVAMLAAP-AVSAHAEEQCSQAGGATCPNCLCCSKFGCGTSDYCGTGCQSQ 59

DB 1 mralavvamvparpfiaaahaeqcgagavcpnclccskfgwgcgtsdycgagcgsc 60

QY 60 N-----GCSGCTPVPTPSGGVSSIISQSLFDQMLLRNDAACLAKEFYNYGAFVA 112

DB 61 srlrrrrpdasgg-----ggsgvasivsrifdlmlrrndaacpasnfytadava 112

QY 113 AANSFSGFATTGSTDYKKREVAFLAQTSHETTGWPTAPDGPYSGWYCFNOR-GAITS 171

```

Db 113 aasafpfaaagdadtntkrevaaflactshettggwatapdgytwgycfkeengagpd 172
QY 172 YCTPSSQPCAPGKKYFGRGPIQISHNYYGPAQOATGTDLLNNPDLVADATVSPKAL 231
Db 173 ycqsagwpcaaagkkygrgpiqlisynfnypaggaigadllgdpdlvasdatvsfdaf 232
QY 232 WFWMTQSPKSSHDVITGRWSPSGADQAGRVPGYGVITNIINGGLECGRGQDGRVADR 291
Db 233 wfwmtqspkpcsnavatgwtpsadqragrvpgygvitniingglecghgeddriadr 292
QY 292 IGFYKRYCDLLGVSYGNDLCYNORPEA 319
Db 293 igfykrycdilgvsganldcysqrpsa 320

```

RESULT 5

AAR67969
ID AAR67969 standard; Protein; 336 AA.

XX AAR67969;

DT 13-AUG-1995 (first entry)

XX Rice chitinase.

XX Chitinase; transgenic plant; disease resistance;
KW crop improvement; tobacco; Nicotiana tabacum; plant defense;
KW fungus pathogen; Cercospora nicotinae;
KW Thanatephorus cucumeris.

XX Oryza sativa.

OS WO9502319-A.

PN 26-JAN-1995.

PD 15-JUL-1994; 94WO-US07815.

XX 16-JUL-1993; 93US-0093372.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Dixon RA, Lamb CJ, Maher EA, Zhu Q;

PI WPI; 1995-067090/09.

XX N-PSDB; AAQ81346.

XX Transgenic plants contg. several plant defence associated
PT proteins - have increased resistance to plant pathogens when
PT grown in crops as a food source

XX Disclosure; Page 31-32; 45pp; English.

XX The Sphi fragment of rice chitinase RCH10 gene (given in AAQ81346) and
CC an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were
CC incorporated into vectors for co-expression in transgenic tobacco,
CC resulting in improved resistance to Cercospora nicotinae and
CC Thanatephorus cucumeris fungal infection.

XX Sequence 336 AA;

Query Match 73.7%; Score 1301.5; DB 16; Length 336;
Best Local Similarity 72.3%; Pred. No. 1.8e-99;
Matches 237; Conservative 27; Mismatches 47; Indels 17; Gaps 4;

QY 1 MRGVVVVWMLAAAF-AVSAHAEOCGSAGGATCPNCLCCSKFGCGTSDYCGTCGCSQC 59

Db 1 mralavamvarpfiaaahaeqcgsgagavcpncldcsqfgwgstsdycgagcgsc 60

QY 60 N-----GCSGTPVPVPTSGGVSIIISQSLFDQMLLRNDAACLAAGFYNGAFVA 112

```

Db 61 srirrrrdpdsagg-----ggsgvasivsrslfmlhlhrndaacpasnfytadafa 112
QY 113 AANSFSGFATTGSDVKKREVAFLAQTSHETTGWTFADPGYSGYCENOEER-GATSD 171
Db 113 aasafpfaaagdadtntkrevaaflactshettggwatapdgytwgycfkeengagpd 172
QY 172 YCTPSSQPCAPGKKYFGRGPIQISHNYYGPAQOATGTDLLNNPDLVADATVSPKAL 231
Db 173 ycqsagwpcaaagkkygrgpiqlisynfnypaggaigadllgdpdlvasdatvsfdaf 232
QY 232 WFWMTQSPKSSHDVITGRWSPSGADQAGRVPGYGVITNIINGGLECGRGQDGRVADR 291
Db 233 wfwmtqspkpcsnavatgwtpsadqragrvpgygvitniingglecghgeddriadr 292
QY 292 IGFYKRYCDLLGVSYGNDLCYNORPEA 319
Db 293 igfykrycdilgvsganldcysqrpsa 320

```

RESULT 6

AAB11488

ID AAB11488 standard; protein; 323 AA.

XX AAB11488;

AC 02-MAR-2001 (first entry)

DT Wheat chitinase protein homologous to rye chitinase.

DE Wheat; chitinase; low temperature expression; hardened; plant;
XX snow mould resistance; psychophilic plant pathogen; rye.

XX Triticum aestivum.

OS JP2000270866-A.

PN 03-OCT-2000.

XX 25-MAR-1999; 99JP-0081694.

XX 25-MAR-1999; 99JP-0081694.

XX (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.

PA WPI; 2001-027417/04.

XX New low temperature expression chitinase gene for producing a plant
PT grade highly resistant to psychophilic plant pathogenic microbes
XX Claim 4; Fig 2; 11pp; Japanese.

XX This invention describes novel wheat chitinase genes. The invention also
CC describes a method for the isolation of a low temperature expression
CC chitinase gene in which the mRNA is extracted from a fully hardened
CC autumn wheat PI173438 (of high snow mould resistance). The genes are
CC useful for creating a plant grade, highly resistant to psychophilic plant
CC pathogenic microbes.

XX Sequence 323 AA;

Query Match 73.3%; Score 1294.5; DB 22; Length 323;
Best Local Similarity 71.0%; Pred. No. 6.6e-99;
Matches 223; Conservative 34; Mismatches 48; Indels 9; Gaps 1;

QY 5 VVVWMLAAAF-AVSAHAEOCGSAGGATCPNCLCCSKFGCGTSDYCGTCGCSQC 64

Db 12 vlvvvlaaaavtpataeqcgagagkacdlccsqfsgttdsdycgpcqsgctgcgg 71

QY 65 GTPVPVPTSGGVSIIISQSLFDQMLLRNDAACLAAGFYNGAFVAAANSFSGFATG 124

Db 72 g-----gggvasivsrldlferflhrndaaclargfytydaflaaagafpfgtg 122

QY 125 STDVKKREVAALAQTSHTTGGWTPADGPYSWGYCFNQRGATSDYCTPSQWPCAPG 184
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 123 dldtkrevaaafgqtshtttgwtapdgp:swgycfkqeggsppsycdgsadwpcapg 182
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 185 KXYFGRGPTQISHNNYNGPAGQAIGTDLNNPDLVADATVSKTALWFWMTPOSXPKSS 244
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 183 kqygrgpiqlthnyyngpagraigvdl:lnnpdlvatdptvarktafwmtqsknpsc 242
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 245 HDVITGRWSPSGADQAAGRPVGYGVITNIINGLEGCRGQDGRVADRIGFYKRYCDLLGV 304
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 243 hdvitglwtpardsaagrvpygvitnvngiecmgmgndkvadrigfykrycdifgi 302
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 305 SYGDNLDYCNQRPF 318
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 303 gygnnldcynqlsf 316
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||

RESULT 7
AAB67444
ID AAB67444 standard; Protein; 336 AA.
XX AAB67444:
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a rice chitinase designated RCH10.
XX
KW Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase;
KW Xanthomonas; plant pathogen; Br11 protein; RCH10 protein.
XX
OS Oryza sp.
XX
PN WO200109283-A2.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-US20714.
XX
PR 28-JUL-1999; 99US-0363313.
XX
PA (REGC) UNIV CALIFORNIA.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Ronald P, He Z, Chory J, Lamb C, Li J;
XX
DR WPI; 2001-159858/16.
DR N-PSDB; AAF54983.
XX
PT Chimeric plant receptors comprising a polynucleotide encoding a RKK
PT receptor containing a heterologous extracellular domain and a kinase
PT domain from a Xa21 polypeptide, useful for modulating plant responses
PT to pathogens -
XX
PS Disclosure; Page 45-46; 47pp; English.
XX
CC The present sequence represents a chitinase designated RCH10. The
CC specification describes chimeric receptors which are used for modulating
CC plant responses to pathogens. The receptors comprise a heterologous
CC extracellular domain (e.g. from a Br11 protein or RCH10 protein) and
CC a kinase domain (e.g. from disease resistance protein Xa21). The Xa21
CC gene is a member of disease resistance genes referred to as RKK genes.
CC When Xa21 is present in a transgenic plant, it confers resistance to
CC Xanthomonas spp.. The plant receptors containing heterologous domains
CC are useful for modulating plant responses to pathogens including viruses,
CC bacteria, nematodes, fungi or insects. The nucleic acids can be used to
CC confer desired traits on essentially any plant.
SQ Sequence 336 AA;

Query Match 73.2%; Score 1291.5; DB 22; Length 336;
Best Local Similarity 71.6%; Pred. No. 1.2e-98;
Matches 235; Conservative 27; Mismatches 49; Indels 17; Gaps 4;

QY 1 MRGVVVVAMLAAP-AVSAHAECQSQAGATCPNCLCCSKFQFCGTTSDYCGTCQSQSC 59
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 1 mralavvamvarpfiaaavhaeqsgagavcpcnclccsfqwcgtsdycgagcsgc 60
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 60 N-----GCSGTPVPVTPPSGGVSSIIISQSLFDQMLLHRRNDAACLAKEFYNYGAFA 112
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 61 srllrrrrpdasgg-----ggsgvasivsrslfdmlhlhrndaacpasnfitydafva 112
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 113 AANSFSGFATITGTDYKREVAALAQTSHTTGGWTPADGPYSWGYCFNQRGATSD 171
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 113 aasafgfaagadatkrevaaflaqtshettggwatapdpytwgycfkeengagpd 172
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 172 YCTPSSQWPCAPGKYPGRGPIQISHNNYNGPAGQAIGTDLNNPDLVADATVSKTAL 231
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 173 ycdgsaqwpcacgkkyvgrgpiqlsynfnypgaggaigadllgpdldvasdatvsfdatf 232
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 232 WFWMTPOSXPKSSHDVITGRWSPSGADQAAGRPVGYGVITNIINGLEGCRGQDGRVADR 291
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 233 wfwmtposxpkpscnavatgqwtpsaddqragrvpygvitniikgglecghgdriadr 292
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
QY 292 IGFYKRYCDLLGVSYGDNLDYCNQRPFA 319
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 293 igfykrycdllgvsyganldcysgrpsa 320
| : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||

RESULT 8
AAR15841
ID AAR15841 standard; Protein; 329 AA.
XX AAR15841:
XX
DT 19-MAR-1992 (first entry)
XX
DE Basic chitinase 48 from clone lambdaCHN17.
XX
KW Vacuole; targeting; chitinase; glucanase; signal; resistance;
KW pharmaceutical; hormones; expression; secretion; extracellular.
XX
OS Nicotiana tabacum L. C.v. Havana 425.
XX
FH Key Location/Qualifiers
FT Region 1..148
FT /label= exon1_prod.
FT Region 149..199
FT /label= exon2_prod.
FT Region 200..329
FT /label= exon3_prod.
FT Peptide 318..329
FT /label= sig_peptide
FT /note= "used as vacuole targeting peptide"
XX
PN EP462065-A.
XX
PD 18-DEC-1991.
XX
PF 06-JUN-1991; 91EP-0810430.
XX
PR 15-JUN-1990; 90CH-0002007.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI Bollner T, Nauhaus JM, Ryals J;
XX
DR WPI; 1991-371028/51.
DR N-PSDB; AAQ15147.
XX
PT DNA sequence encoding vacuole targeting peptide - esp. signal
PT region of tobacco chitinase or glucanase gene, and derived
PT recombinant DNA, vectors, etc. functional in plants
PS Disclosure; Page 64-68; 81pp; English.
XX

RESULT 12

AA07513
ID AAB07513 standard; Protein; 324 AA.
XX
AC AAB07513;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of an extracellular chitinase.
XX
KW Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;
KW plant resistance; pathogenic fungi; fungal resistant plant.
XX
OS Nicotiana sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
XX
PN US6087560-A.
XX
PD 11-JUL-2000.
XX
PF 18-FEB-1997; 97US-0801563.
XX
PR 19-APR-1993; 93US-0047413.
PR 29-JAN-1991; 91US-0647831.
XX
FA (UYLE-) RIJKSUNIV LEIDEN.
FA (MOGE-) MOGEN INT NV.
XX
PI Cornelissen BJC, Melchers LS, Meulenhoff EJS, Sela-buuriage MB;
PI Vloemans AA, Woloshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
XX
DR WPI; 2000-498214/44.
DR N-PSDB; AAA58910.
XX

New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici - -
Example 4; Fig 2A-B; 42pp; English.
XX
CC The present sequence represents an extracellular chitinase. The
CC specification describes transgenic plants which express a chitinase
CC gene and a glucanase gene. The expression of the chitinase and
CC beta-1,3-glucanase genes produces an antifungal effect. The transgenic
CC plants are useful for improving plant resistance to pathogenic fungi.
CC The recombinant polynucleotides and the process are useful for
CC producing fungal resistant plants.
XX
SQ Sequence 324 AA;

Query Match 70.9%; Score 1252; DB 21; Length 324;
Best Local Similarity 71.8%; Pred. No. 2.1e-95;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;
Oy 8 AMLAARFVSAHAECGSGAGNCPNCLCSKFGCTTSDYCGTG-CQSQCGNCSCGT 66
Db 11 SILLFLLLSAEGCSGAGGACASGLCCSKFGWGTNDYCGNCGSQCGP--gpt 68
Oy 67 PVPVPTSGGVSSITISQSLFDQMLLRNDAACLAAGFYNYGAFVAAANSFSGFATTGST 126
Db 69 P-----pgggdlsliissmfdqmlkhrndnacgkgfysynafinaarsfgfgtsdgt 123
Oy 127 DVKREVAFLAQTSHEFTGWPADPGYSGWYCFNCGERGATSDYCPSSQWFCAPGK 186
Db 124 tarkreiaaafagtshttgwatadpyagwycwlrqcspgdyctpsgqwcpcaprk 183
Oy 187 YFGRGPIQISHNYPGAGACIGDRLNPNPLVASDAIVSKTALFWMTQSPKPSHD 246
Db 184 yfgr-gpiqishnynypgcaigavdlhnpdlvatdpyvisfkisalwfwmtqspkpschd 243

Oy 247 VITGRWSPSGADQAAAGRVPGVGTITNIINGLECGRGODGRVADRIGFKRYCDLLGYSY 306
Db 244 viiqrwqssadraanrpgfgvitiinglegcrgtdsrvtqdrigfryrcsilgvsp 303
Oy 307 GDNLDYCNORPF 318
Db 304 gdnldcgnqrsf 315

RESULT 13

AA020822
ID AAR20822 standard; Protein; 328 AA.
XX
AC AAR20822;
XX
DT 16-MAY-1992 (first entry)
XX
DE Sequence of endochitinase precursor.
XX
KW Pest-resistant plant; transformed plant; fungi; insect; bacteria;
KW nematode.
XX
OS Tomato and tobacco.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= signal
FT Peptide 25..69
FT /label= cleavage
XX
PN WO9201792-A.
XX
PD 06-FEB-1992.
XX
PF 24-JUL-1991; 91WO-FR00607.
XX
PR 24-JUL-1990; 90FR-0009460.
XX
FA (SNFI) SANOFI SA.
FA (ERAP) SOC NAT ELF AQUITAINE.
XX
PI Dubois M, Grison R, Leguay JJ, Pignard A, Toppan A;
XX
DR WPI; 1992-064950/08.
DR N-PSDB; AAQ21193.
XX
PT New recombinant protein with endo chitinase activity - also DNA
PT encoding it and plants which express it, resistant to fungi,
PT insects, bacteria and nematodes.
XX
PS Example; Fig 4; 82pp; French.
XX

The inventors claim a new recombinant gene which codes for a protein with endochitinase activity, or its precursor (see AAQ21007). The coding part of the gene contains at least the 5' part of DNA for tomato endochitinase and at least the 3' part of DNA for the tobacco enzyme (DNA can be genomic or cDNA, but at least one intron is pref. present). The recombinant gene includes the 35S promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of Agrobacterium tumefaciens.

SQ Sequence 328 AA;

Query Match 68.1%; Score 1202.5; DB 13; Length 328;
Best Local Similarity 67.8%; Pred. No. 2.6e-91;
Matches 213; Conservative 38; Mismatches 52; Indels 11; Gaps 5;
Oy 7 VAMLAARFVSAHAECGSGAGGATCPNCLCSKFGCTTSDYCGTG-CQSQCGNCSCGG 65
Db 15 lviisaal-----aqncqsggqgkvccasgqccskfgwcgntndhcgsgncsqg---cpgg 66

QY 66 TPVPVPTPGGGVSSIIISOSLFQDMLLRNDAACLAK-GFYNYGAFVAAANSFSGFATG 124
 Db 67 gp9pgpv-tggdlgsvisnsmtdqmlkhrnenscggknufsynafitaarsfpgfgtsg 125
 QY 125 STDVKKREVAALAQTSHTTGGWPTAPDGPYSWGVCFNQERGATSDYCTPSSOWPCAPG 184
 Db 126 dlnarkrelaafagtshtetgwpapdgpfawgycfllrerngpdyccspssqwpcapg 185
 QY 185 KYFGRGPIQISHNINYPGAGQAIGTDLLNPDIVASDATVSFKTALWFWMTPQSPKPS 244
 Db 186 rkyfgrgpiqishnynypcgraigvdlldnplvatdvisfktaiwfwmtpqspkpsc 245
 QY 245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGLECGRGDGRVADRIGFYKRYCDLLGV 304
 Db 246 hdvlgwrwpsagdranrlpgfvgitniingglecrgndrnrvqdrigrfyrccgilv 305
 QY 305 SYGDNLDYCNQRP 318
 Db 306 spgdnldcgnqrsf 319

RESULT 14
 AAR56860 standard; Protein; 329 AA.
 XX AAR56860;
 AC AAR56860;
 XX
 DT 17-FEB-1995 (first entry)
 DE Endochitinase precursor coding sequence.
 DE oxalic acid degradation; oxalate oxidase; selection marker;
 KW tomato endochitinase; tobacco endochitinase; precursor;
 KW pathogen resistance; plant cell selection.
 XX
 OS Lycopersicon esculentum.
 OS Nicotiana tabacum.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24 /label= pre-sequence
 FT Region 25..75 /label= pro-sequence
 FT Protein 76..329 /label= endochitinase
 FT
 XX WO9413790-A.
 PN
 XX
 PD 23-JUN-1994.
 XX
 PF 07-DEC-1993; 93WO-FR01203.
 XX
 PR 07-DEC-1992; 92FR-0014721.
 XX
 XX (SNFI) ELF SANOFI.
 PA (BRAP) SOC NAT ELF AQUITAINE.
 XX
 XX Grezes-Besset B, Grison R, Pignard A, Schneider M;
 PI WPI; 1994-217870/26.
 XX N-PSDB; AAQ68352.
 DR
 DR Use of gene encoding oxalic acid degrading enzyme - for plant
 PT cell selection, esp. gene coupled to gene-encoding protein
 PT conferring pathogen resistance
 XX
 PS Disclosure; Page 34-37; 64pp; French.
 XX
 CC The sequence coding for wheat germin, a protein induced during
 CC germination of wheat, is a preferred example of DNA coding for a
 CC protein able to degrade oxalic acid. Such DNA can be coupled to a
 CC sequence of interest, e.g. one coding for enzymes which confer
 CC resistance to pathogens (esp. endochitinases). Plant calli which

CC have been successfully transformed by the sequences are selected
 CC by their ability to grow on oxalic acid-contg. medium. AAR56860 is
 CC a known sequence of a precursor of endochitinase; the sequence was
 CC previously disclosed in WO9201792.
 XX
 SQ Sequence 329 AA;
 Query Match 68.1%; Score 1202.5; DB 15; Length 329;
 Best Local Similarity 67.8%; Pred. No. 2.6e-91;
 Matches 213; Conservative 38; Mismatches 52; Indels 11; Gaps 5;
 QY 7 VAMLAARFAVAHAECGSGAGGATCPNCLCCSKFPCGTTSDYCGTG-CQSOCCSGSG 65
 Db 16 lvllsaal-----aqncsgsggdkvcasgqccskfgwcnthdcsnccsq---cp9g 67
 QY 66 TPVPVPTPGGGVSSIIISOSLFQDMLLRNDAACLAK-GFYNYGAFVAAANSFSGFATG 124
 Db 68 gp9pgpv-tggdlgsvisnsmfdqmlkhrnenscggknufsynafitaarsfpgfgtsg 126
 QY 125 STDVKKREVAALAQTSHTTGGWPTAPDGPYSWGVCFNQERGATSDYCTPSSOWPCAPG 184
 Db 127 dlnarkrelaafagtshtetgwpapdgpfawgycfllrerngpdyccspssqwpcapg 186
 QY 185 KYFGRGPIQISHNINYPGAGQAIGTDLLNPDIVASDATVSFKTALWFWMTPQSPKPS 244
 Db 187 rkyfgrgpiqishnynypcgraigvdlldnplvatdvisfktaiwfwmtpqspkpsc 246
 QY 245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGLECGRGDGRVADRIGFYKRYCDLLGV 304
 Db 247 hdvlgwrwpsagdranrlpgfvgitniingglecrgndrnrvqdrigrfyrccgilv 306
 QY 305 SYGDNLDYCNQRP 318
 Db 307 spgdnldcgnqrsf 320

RESULT 15
 AAW00186
 ID AAW00186 standard; Protein; 317 AA.
 XX
 AC AAW00186;
 XX
 DT 18-OCT-1996 (first entry)
 DE American elm chitinase-like protein.
 XX
 KW Clone pH52; chitinase; american elm; fungus; Ophiostoma ulmi;
 KW dutch elm disease; E. coli; chitinase-like protein;
 KW fungal infection.
 XX
 OS American elm.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21 /note= "signal peptide"
 FT Protein 22..317 /note= "Mature chitinase-like protein"
 FT
 XX US5539095-A.
 PN
 XX 23-JUL-1996.
 PD
 XX 04-AUG-1994; 94US-0286020.
 XX
 XX 04-AUG-1994; 94US-0286020.
 XX
 PA (UNMS) UNIV MICHIGAN STATE.
 XX
 XX Hajela RK, Sticklen MB;
 XX WPI; 1996-353879/35.
 DR N-PSDB; AAT33325.

QY 1 MRGVVVVLAALAAAF-AVSAHAECGSGAGGATCPNCLCCSKFGCGTTSYDYGCGCQSQ 59
Db 1 MRALAVVAVARFLAAVIAECGSGAGGATCPNCLCCSKFGCGTTSYDYGCGCQSQ 60
QY 60 N-----GCSGGTTPVPTPSGGGVSSISQSLFQDMLLRNDAAKLAKGFYNYGAFVA 112
Db 61 SRLRRRPDASGG-----GGSGVASIVSRSLFQDMLLRNDAAKLAKGFYNYGAFVA 112
QY 113 AANSFSGFATGSDTVKKREVAALFAOTSHTTGGWPTAPDPGYSWGYCFNQER-GATSD 171
Db 113 AASAFPFGAAGADATNKKREVAALFAOTSHTTGGWPTAPDPGYSWGYCFNQER-GATSD 172
QY 172 YCTPSSQWPCAPGKKYGRGFIQISHNINYPAGOAIGTDLNNPDLVASDATVSFKTAL 231
Db 173 YCQSAQWPCAPGKKYGRGFIQISHNINYPAGOAIGTDLNNPDLVASDATVSFKTAL 232
QY 232 WFWMTQSPKPSHDVITGRWSPGSAQAAGRVPGYGVITNINGLGCGQDGRVADR 291
Db 233 WFWMTQSPKPSHDVITGRWSPGSAQAAGRVPGYGVITNINGLGCGQDGRVADR 292
QY 292 IGFYKRYCDLGVSGYDNLDCYNORPFA 319
Db 293 IGFYKRYCDLGVSGYDNLDCYNORPFA 320

RESULT 4

US-07-791-931-6
; Sequence 6, Application US/07791931C
; Patent No. 6133567
; GENERAL INFORMATION:
; APPLICANT: RaiXhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07791,931C
; PRIORITY FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-07-791-931-6

Query Match 71.2%; Score 1257; DB 4; Length 310;
Best Local Similarity 73.7%; Pred. No. 5.9e-107;
Matches 224; Conservative 26; Mismatches 46; Indels 8; Gaps 3;

QY 15 VSAHAECGSGAGGATCPNCLCCSKFGCGTTSYDYGCGCQSQCGSGTTPVPTPS 74
Db 5 LSASAEQCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGCQSQCGSGTTPVPTPS 74
QY 75 GGVVSSISQSLFQDMLLRNDAAKLAKGFYNYGAFVAANFSFGFATGSDTVKKREVA 134
Db 58 GDLGSLISSMFDQMLKRNDAACQKGFYSYNAPINAAFSFGFATGSDTVKKREVA 117
QY 135 AFLAOTSHTTGGWPTAPDPGYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYGRGFIQ 194
Db 118 AFLAOTSHTTGGWPTAPDPGYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYGRGFIQ 177
QY 195 ISHNYNGPAGAIQWDLNNPDLVASDATVSFKTALFWMTQSPKPSHDVITGRWSP 254
Db 178 ISHNYNGPAGAIQWDLNNPDLVASDATVSFKTALFWMTQSPKPSHDVITGRWSP 237
QY 255 SGADQAGRVPGYGVITNINGLGCGQDGRVADRIGFYKRYCDLGVSGYDNLDCYN 314
Db 238 SSADRAANRLPGVGVITNINGLGCGQDGRVADRIGFYKRYCDLGVSGYDNLDCYN 297
QY 315 QRF 318
Db 298 QRF 301

RESULT 5
US-08-047-413-11
; Sequence 11, Application US/08047413
; Patent No. 5670706
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Feerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/047,413
; FILING DATE: 19-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-047-413-11

Query Match 70.9%; Score 1252; DB 1; Length 324;
Best Local Similarity 71.8%; Pred. No. 1.8e-106;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;
QY 8 AMLAAAFVSAHAECGSGAGGATCPNCLCCSKFGCGTTSYDYGCGCQSQCGSGT 66
Db 11 SILFSLILLASAEQCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGCQSQCGSGT 68
QY 67 PVEPVTTPSGGVSSISQSLFQDMLLRNDAAKLAKGFYNYGAFVAANFSFGFATGSD 126
Db 69 P-----PGGDLGSLISSMFDQMLKRNDAACQKGFYSYNAPINAAFSFGFATGSD 123
QY 127 DVKKREVAALFAOTSHTTGGWPTAPDPGYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
Db 124 TARKREIAFAAQTSHETTGGWATAPDPGYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 183
QY 187 YFGRGPIQISHNINYPAGOAIGTDLNNPDLVASDATVSFKTALFWMTQSPKPSHD 246
Db 184 YFGRGPIQISHNINYPAGOAIGTDLNNPDLVASDATVSFKTALFWMTQSPKPSHD 243

QY 247 VTGRWSPSADQAAGRVPGYGVITNIINGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
Db 244 VTIGRWQPSADRAANRLPFGVITNIINGLECGRGTDSDRVQDRIGFYRRYCSILGVSP 303
QY 307 GDNLCYNORPF 318
Db 304 GDNLCGNORSE 315

RESULT 6
US-08-229-050-11
; Sequence 11, Application US/08229050
; Patent No. 6066491
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-229-050-11

Query Match 70.9%; Score 1252; DB 3; Length 324;
Best Local Similarity 71.8%; Pred. No. 1.8e-106;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;

QY 8 AMLAAAFVASHACQSGAGGATCPNCLCCSKFGCTGTSYDYGTCG-CQSQCNCGSGGT 66
Db 11 SLFLSLLLSASACQSGAGGATCGLCCSKFGCTGNTDYCGPNCQSQCPG--GPT 68
QY 67 PVPYPTSGGGVSSIIQSLFDQMLLHNDAACLAKGFYNYGAFVAAANSFGATGTGST 126

Db 69 P-----PGGDLGSLSSSMFDQMLKHRNDNACQKGFYSYNAFINAARSFPGFGTSGDT 123
QY 127 DVKKREVAFLAQTSHTTGGNPTAPDGPYSWGYPNQERGATSDYCTPSSQWPCAPGKK 186
Db 124 TARKREIAFAAQTSHETTTGGWATAPDGPYAWGYCWLREQCCSGDYCTPSGOWPCAPGRK 183
QY 187 YFGRGPQIQISHNYNYPGAGQATGTDLLNNPDLVASDATYSEKTALEWFWMTQSPKPSHSD 246
Db 184 YFGRGPQIQISHNYNYPGCGRAIGVDLLNNPDLVATDPVISEKALSALWFWMTQSPKPSCHD 243
QY 247 VTGRWSPSADQAAGRVPGYGVITNIINGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
Db 244 VTIGRWQPSADRAANRLPFGVITNIINGLECGRGTDSDRVQDRIGFYRRYCSILGVSP 303
QY 307 GDNLCYNORPF 318
Db 304 GDNLCGNORSE 315

RESULT 7
US-08-801-563-11
; Sequence 11, Application US/08801563
; Patent No. 6087560
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,563
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,413
; FILING DATE: 19-APR-1993
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-801-563-11

Query Match 70.98; Score 1252; DB 3; Length 324;
Best Local Similarity 71.88; Pred. No. 1.8e-106;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;

QY 8 AMLAAFAVSAHAECQAGGATCPNCCSKFGCGTTSYDYGTCG-CQSCQNCSCSGT 56
DB 11 SLLSLLLSASAECQAGGATCPNCCSKFGCGTTSYDYGTCG-CQSCQNCSCSGT 56
QY 67 PVPVPTGGVSSIIISQSLFDQMLLHRNDACLAAGYNYGAFVAAANSFGFATTG 126
DB 69 P-----PGGDLGSISSSMEDQMLKHNNDACQCGKGYSYNAFTNAARSFPFGTSGDT 123
QY 127 DVKREVAFAAQTSHETTGWPTAPDGPYSGYCFNCGRATSDYCTPSSQWPCAPGKK 186
DB 124 TARKREIAAFAQTSHETTGWPTAPDGPYSGYCFNCGRATSDYCTPSSQWPCAPGKK 183
QY 187 YFGRPIQISHNYNGPAGQATGTDLLNPDIVASDATVSKTALFWMTPOSPPSSHD 246
DB 184 YFGRPIQISHNYNGPAGRAIGVDLLNPDIVATDPVISEKSALEWMTPOSPPSSHD 243
QY 247 VITGKSSGDAQAGRPVGGVITNIINGLCCGRGQDGRVADRIGYKRYCDLLGYSY 306
DB 244 VITGRWQSSADRAANRLPGFVITNIINGLCCGRGQDGRVADRIGYKRYCISLGVSP 303
QY 307 GNDLCYNORPF 318
DB 304 GNDLCGNORSHF 315

RESULT 8
US-07-704-288C-6
; Sequence 6, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; TITLE OF INVENTION: DEFENSE ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8999
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-07-704-288C-6

Query Match 70.68; Score 1246.5; DB 1; Length 310;
Best Local Similarity 73.78; Pred. No. 5.4e-106;
Matches 224; Conservative 26; Mismatches 45; Indels 9; Gaps 4;

QY 16 VSAHAECQAGGATCPNCCSKFGCGTTSYDYGTCG-CQSCQNCSCSGT 74
DB 6 LSAAECQAGGATCPNCCSKFGCGTTSYDYGTCG-CQSCQNCSCSGT 58
QY 75 GGVSSIIISQSLFDQMLLHRNDACLAAGYNYGAFVAAANSFGFATTG 134
DB 59 GGDGSISSSMEDQMLKHNNDACQCGKGYSYNAFTNAARSFPFGTSGDT 118
QY 135 AFLAQTSHETTGWPTAPDGPYSGYCFNCGRATSDYCTPSSQWPCAPGKKYFGRGPIQ 194
DB 119 AFFAQTSHETTGWPTAPDGPYSGYCFNCGRATSDYCTPSSQWPCAPGKKYFGRGPIQ 178
QY 195 ISHNTNYGPAQATGTDLLNPDIVASDATVSKTALFWMTPOSPPSSHDVITGRWSP 254
DB 179 ISHNTNYGPAQATGTDLLNPDIVATDPVISEKSALEWMTPOSPPSSHDVITGRW-P 237
QY 255 SGADQAGRPVGGVITNIINGLCCGRGQDGRVADRIGYKRYCDLLGYSY 314
DB 238 SSADRAANRLPGFVITNIINGLCCGRGQDGRVADRIGYKRYCISLGVSPGNDLCGN 297
QY 315 QRPFF 318
DB 298 QRSF 301

RESULT 9
US-08-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids

	Query Match	68.1%;	Score 1202.5;	DB 2;	Length 329;
	Best Local Similarity	67.6%;	Pred. No. 5.9e-102;		
	Matches 213; Conservative	38;	Mismatches 52;	Indels 11;	Gaps 5;
QY	7 VAMLAAFVSAHAHBCGSGAGATCPNCLCCSKFPGTTSDDYCGTG-CQSQCNCSSGG	65			
	: : : : : :	:	:	:	:
DB	16 LVLLSAL-----AQNCGSGGGKVCASQCSKFGEWCNTDHCNGMCQQSQ---- <td>67</td> <td></td> <td></td> <td></td>	67			
QY	66 TVPVPTPSGGGVSSIISGSLEDFQMLLHRNDAACTAK-GFYNYGFVFAAANSFSFGATTG	124			

Db 10 VAYLLFSLVLAALQNGSGGGKACASQCCSKFGWCGTNDYCGSGNCQSQ--C 66
QY 63 SGGTVPVPTSSGGVSSIIQSLEFQMLLHRNDAAKAGFYNGAFVAAANSFSGEAT 122
Db 67 PGGGPGPGP--GGDLGSAISNMFQMLKHNENSCOGKFNYSYNAFINAARSFPFGGT 123
QY 123 TGSTVDKKREVAALFAQTSHETTTGGWPTAPDGPYSGWYCFNOCERGATSDYCTPSSQWPCA 182
Db 124 SEDIINARKEIAAFAQTSHETTTGGWASAPDGPYAWGYCFLEGRNPGDYCPSSQWPCA 183
QY 183 PGKKGFGPGPIQISHNINYPGAGQAIGTDLNPNPLVADATVSKTALFWFMTTQSPKP 242
Db 184 PGKKGFGPGPIQISHNINYPGCGRAIADVLLNPNPLVATDPVISEKTALFWFMTTQSPKP 243
QY 243 SSHDVTGRWSPGADQAAGRPVPGVITNIINGGLECGRGODGRVADRIGFYKRYCSDL 302
Db 244 SCHEDVIIGRWPNSSADRAANRLPGFVITNIINGGLECGRGTDNRVQDRIGFYRYCSDL 303
QY 303 GVSYGNDLDCYNORPF 318
Db 304 GVTPGNDLDCYNORWF 319

RESULT 14

US-08-379-259-8
; Sequence 8, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-8

Query Match 68.1%; Score 1202; DB 1; Length 330;
Best Local Similarity 68.7%; Pred. No. 6.6e-102;

Matches 217; Conservative 31; Mismatches 58; Indels 10; Gaps 4;
QY 7 VAMLAFAAV---SAFAEQCGSAGGATPCNLCCKSKFGCGTTSDYCGTG-CQSQCNCG 62
Db 10 VAYLLFSLVLAALQNGSGGGKACASQCCSKFGWCGTNDYCGSGNCQSQ--C 66
QY 63 SGGTVPVPTSSGGVSSIIQSLEFQMLLHRNDAAKAGFYNGAFVAAANSFSGEAT 122
Db 67 PGGGPGPGP--GGDLGSAISNMFQMLKHNENSCOGKFNYSYNAFINAARSFPFGGT 123
QY 123 TGSTVDKKREVAALFAQTSHETTTGGWPTAPDGPYSGWYCFNOCERGATSDYCTPSSQWPCA 182
Db 124 SEDIINARKEIAAFAQTSHETTTGGWASAPDGPYAWGYCFLEGRNPGDYCPSSQWPCA 183
QY 183 PGKKGFGPGPIQISHNINYPGAGQAIGTDLNPNPLVADATVSKTALFWFMTTQSPKP 242
Db 184 PGKKGFGPGPIQISHNINYPGCGRAIADVLLNPNPLVATDPVISEKTALFWFMTTQSPKP 243
QY 243 SSHDVTGRWSPGADQAAGRPVPGVITNIINGGLECGRGODGRVADRIGFYKRYCSDL 302
Db 244 SCHEDVIIGRWPNSSADRAANRLPGFVITNIINGGLECGRGTDNRVQDRIGFYRYCSDL 303
QY 303 GVSYGNDLDCYNORPF 318
Db 304 GVTPGNDLDCYNORWF 319

RESULT 15

US-07-791-931-7
; Sequence 7, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Phaseolus vulgaris
US-07-791-931-7

Query Match 67.0%; Score 1183; DB 4; Length 328;

Best Local Similarity 67.1%; Pred. No. 3.5e-100;

Matches 212; Conservative 36; Mismatches 54; Indels 14; Gaps 4;

QY 3 GVVVAMLAFAVSAHAEOCGSAGGATPCNLCCKSKFGCGTTSDYCGTGCGSQCNCG 62
Db 14 GVVVMLLVG---GSYGEQCGRAGGALCPGGNCCSQFGWCGSTTDYCGPGCQCGG- 68
QY 63 SGGTVPVPTSSGGVSSIIQSLEFQMLLHRNDAAKAGFYNGAFVAAANSFSGEAT 122
Db 69 ----PSPAPI-----DISALLSRSTFDQMLKHNDCGACPAKGYTYDAFTAAKAYPSFGN 120
QY 123 TGSTVDKKREVAALFAQTSHETTTGGWPTAPDGPYSGWYCFNOCERGATSDYCTPSSQWPCA 182
Db 121 TGDATRKREIAAFLGQTSHTTGGWATAPDGPYAWGYCFVBERN-PSTYCSATPQPPCA 179
QY 183 PGKKGFGPGPIQISHNINYPGAGQAIGTDLNPNPLVADATVSKTALFWFMTTQSPKP 242
Db 180 PGQQTGGRGPIQISWNINYPGCGRAIGVLLNPNPLVATDSVISFSAALFWFMTTQSPKP 239
QY 243 SSHDVTGRWSPGADQAAGRPVPGVITNIINGGLECGRGODGRVADRIGFYKRYCSDL 302
Db 240 SSHDVTISRWTPSSADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGFFKRYCSDL 299
QY 303 GVSYGNDLDCYNORPF 318
Db 300 GVGYGNDLDCYSQTPF 315

Tue May 7 10:52:21 2002

us-09-534-229c-3.ra1

Page 9

Search completed: May 3, 2002, 18:43:05
Job time: 748 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:32:12 ; Search time 88.01 Seconds
(without alignments)
276.101 Million cell updates/sec

Title: US-09-534-229C-3
Perfect score: 1765
Sequence: 1 MRGVVVVAMLAFAVSAHA.....DLLGVSYGDNLDYQNRPFA 319

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

30	1168.5	66.2	327	1	JQ0965	chitinase (EC 3.2.
31	1167.5	66.1	329	2	T06999	chitinase (EC 3.2.
32	1162	65.8	321	2	S57482	chitinase class 1
33	1156	65.5	308	2	JC2253	chitinase (EC 3.2.
34	1154.5	65.4	302	2	T10810	chitinase (EC 3.2.
35	1140	64.6	243	2	JN0884	chitinase (EC 3.2.
36	1125	63.7	266	2	A38664	chitinase (EC 3.2.
37	1120	63.5	243	2	JC5918	chitinase (EC 3.2.
38	1099.5	62.3	318	2	T03026	chitinase (EC 3.2.
39	1071	60.7	263	2	S72528	chitinase (EC 3.2.
40	1045	59.2	264	2	S26625	chitinase (EC 3.2.
41	1022.5	57.9	340	2	S48030	probable chitinase
42	1012	57.3	263	2	S69184	chitinase (EC 3.2.
43	1004	56.9	246	2	S37341	chitinase (EC 3.2.
44	993	56.3	336	1	S18750	chitinase (EC 3.2.
45	966	54.7	275	2	T03032	chitinase (EC 3.2.

ALIGNMENTS

RESULT 1
S38670
chitinase (EC 3.2.1.14) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 20-Feb-1995 #sequence_revision 20-feb-1995 #text_change 22-Jun-1999
C:Accession: S38670
R:Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reisener, H.J.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38670
A:Accession: S38670
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <LIA>
A:Cross-references: EMBL:X76041; NID:g416028; PID:CAA53626.1; PID:g416029
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-320/Domain: plant chitinase homology <PCH>

Query Match	96.1%	Score 1696.5;	DB 2;	Length 320;
Best Local Similarity	95.3%	Pred. No. 6.8e-119;		
Matches	305;	Conservative	9;	Mismatches 5; Indels 1; Gaps 1;
Qy	1	MRGVVVVAMLAFAVSAHAECQCGSQAGGATCPNCLCCSKFSGGTTSDYCGTGCGSQCN	60	
Db	1	MRGVVVVAMLAFAVSAHAECQCGSQAGGATCPNCLCCSKFSGGTTSDYCGTGCGSQCN	60	
Qy	61	GCS-GGTPVPVPTPSGGVSSIISQSLFDQMLLRNDAACLAKEFYNYGAFVAAANSFSG	119	
Db	61	GCSGGGTPVPVPTPSGGVSSIISQSLFDQMLLRNDAACLAKEFYNYGAFVAAANSFSG	120	
Qy	120	FATTGSTDVKKREVAFLAQTSHETGGWPTAPDPYSGWYCFNQERGATSDYCTPSSQW	179	
Db	121	FATTGGADVRRKREVAFLAQTSHETGGWPTAPDPYSGWYCFNQERGAADYCSNPSQW	180	
Qy	180	PCAPGKKYFGRGPTQISHNYNYPGAGQAIGTDLNPNPLVASDATVSPKTLWFWMTPOS	239	
Db	181	PCAPGKKYFGRGPTQISHNYNYPGAGRAIGTDLNPNPLVASDATVSPKTLWFWMTPOS	240	
Qy	240	PKPSSHVDITGRWSPSGADQAAGRVPGYGVITNIINGLEGGRGQDGRVADRIGFYKRYC	299	
Db	241	PKPSSHVDITGRWSPSGADQAAGRVPGYGVITNIINGLEGGRGQDGRVADRIGFYKRYC	300	
Qy	300	DLLGVSYGDNLDYQNRPFA	319	
Db	301	DLLGVSYGDNLDYQNRPFA	320	

RESULT 2
JC2071
chitinase (EC 3.2.1.14) a - rye

Tue May 7 10:52:26 2002

C:Species: Secale cereale (rye)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C:Accession: JC2071
R:Yamagami, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 58, 322-329, 1994
A:Title: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale cereale L.)
A:Reference number: JC2071; MUID:94169514
A:Accession: JC2071
A:Molecule type: protein
A:Residues: 1-302 <VAM>
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-42/Domain: hevein chitin-binding domain homology <HCB>
F:64-302/Domain: plant chitinase homology <PCH>

Query Match 80.3%; Score 1416.5; DB 2; Length 302;
Best Local Similarity 82.1%; Pred. No. 4e-98;
Matches 248; Conservative 26; Mismatches 25; Indels 3; Gaps 3;
QY 21 EQGSGAGGATPCNCLCCSKFSGTSDYCGTGCQSQNGC-SGGTPV-PVPTPS-GGG 77
Db 1 EQGSGAGGATPCNCLCCSKFSGTSDYCGTGCQSQNGC-SGGTPV-PVPTPS-GGG 60
QY 78 VSSIISQSLFDQMLLHRNDACLAAGFYNGAFVAAANSPSGFATGTDVKKREVAFL 137
Db 61 VSSIISQSLFDQMLLHRNDACLAAGFYNGAFVAAANSPSGFATGTDVKKREVAFL 120
QY 138 AOTSHTTGGWPTAPDGYSWGYCFNBERGATSDYCPSSOWPCAPGKFFGRGPIQISH 197
Db 121 AOTSHTTGGWPTAPDGYSWGYCFNBERGATSDYCPSSOWPCAPGKFFGRGPIQISH 180
QY 198 NNYGPAQAGTDLNNPDLVSDATVSEKTLFWMTPOSPPSHDVTGTRWSPSGA 257
Db 181 NNYGPAQAGTDLNNPDLVSDATVSEKTLFWMTPOSPPSHDVTGTRWSPSGA 240
QY 258 DOAAGRPVGYVTNIINGLECGRGDGRVADRIGFYKRYCDLILGVSYGNLDCYNORP 317
Db 241 DOAAGRPVGYVTNIINGLECGRGDGRVADRIGFYKRYCDLILGVSYGNLDCYNORP 300
QY 318 FA 319
Db 301 FA 302

RESULT 3
T04403
chitinase (EC 3.2.1.14) precursor - barley
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
C:Accession: T04403
R:Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
submitted to the EMBL Data Library, September 1993
A:Description: Isolation and characterization of a barley chitinase genomic clone.
A:Reference number: Z15336
A:Accession: T04403
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-318 <IGN>
A:Cross-references: EMBL:U02287; NID:g495304; PID:AAA18586.1; PID:g495305
A:Experimental source: cv. NK1556
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-318/Product: chitinase #status predicted <MAT>
F:20-60/Domain: hevein chitin-binding domain homology <HCB>
F:80-318/Domain: plant chitinase homology <PCH>

Query Match 79.7%; Score 1407.5; DB 2; Length 318;
Best Local Similarity 77.8%; Pred. No. 2e-97;
Matches 249; Conservative 33; Mismatches 35; Indels 3; Gaps 3;

QY 1 MRGVVVVAMLAFAVSAHAECQSQAGATPCNCLCCSKFSGTSDYCGTGCQSQCN 60
Db 1 MRAFLVFAVMA-ATMAVAECQSQAGATPCNCLCCSKFSGTSDYCGTGCQSQCS 58
QY 61 GCGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDACLAAGFYNGAFVAAANSPSG 119
Db 59 GCGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDACLAAGFYNGAFVAAANSPSG 118
QY 120 FATGTDVKKREVAFLAOTSHTTGGWPTAPDGYSWGYCFNBERGATSDYCTPSSOW 179
Db 119 FGTGTDVKKREVAFLAOTSHTTGGWPTAPDGYSWGYCFNBERGATSDYCTPSSOW 178
QY 180 PCAPGKFFGRGPIQISHNNGFYNGAFVAAANSPSGFATGTDVKKREVAFL 239
Db 179 PCAPGKFFGRGPIQISHNNGFYNGAFVAAANSPSGFATGTDVKKREVAFL 238
QY 240 PKSSHDTGTRWSPSGADQAGRPVGYVTNIINGLECGRGDGRVADRIGFYKRYC 299
Db 239 PKSSHDTGTRWSPSGADQAGRPVGYVTNIINGLECGRGDGRVADRIGFYKRYC 298
QY 300 DLGVSYGNLDCYNORPFA 319
Db 299 DLGVSYGNLDCYNORPFA 318
RESULT 4
T03614
chitinase (EC 3.2.1.14) - rice
N:Alternate names: endochitinase
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03614
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice
A:Reference number: S39979; MUID:94049667
A:Accession: T03614
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-323 <NIS>
A:Cross-references: EMBL:D16221; NID:g452232; PIDN:BA03749.1; PID:g500615
A:Experimental source: cv. Nipponbare
C:Genetics:
A:Gene: Cht-1
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-322/Domain: plant chitinase homology <PCH>

Query Match 77.0%; Score 1359.5; DB 2; Length 323;
Best Local Similarity 75.6%; Pred. No. 7.3e-94;
Matches 245; Conservative 27; Mismatches 43; Indels 9; Gaps 4;
QY 1 MRGVVVVAMLAFAVSAHAECQSQAGATPCNCLCCSKFSGTSDYCGTGCQSQCN 60
Db 1 MRALAVVVATAFAVVAVRGEQSGQAGGALCPNCLCCSKYQWCGSTAYCGSQSQCS 60
QY 61 G-CGSGTVPVPTPSG---GVSSIISQSLFDQMLLHRNDACLAAGFYNGAFVAAAN 116
Db 61 GCGGGGTPP---PSGGGGSGVASYVRSFLDQMLLHRNDACPAKNFTYDAFVAAANA 117
QY 117 FSGFATGTDVKKREVAFLAOTSHTTGGWPTAPDGYSWGYCFNBERGATSDYCT 174
Db 118 FSGFATGTDVKKREVAFLAOTSHTTGGWPTAPDGYSWGYCFNBERGATSDYCT 177
QY 175 PSSOWPCAPGKFFGRGPIQISHNNGFYNGAFVAAANSPSGFATGTDVKKREVA 234
Db 178 QSSOWPCAPGKFFGRGPIQISHNNGFYNGAFVAAANSPSGFATGTDVKKREVA 237
QY 235 MTPQSPKPSHVDVTGRWSPSGADQAGRPVGYVTNIINGLECGRGDGRVADRIGF 294
Db 238 MTPQSPKPSHVDVTGRWSPSGADQAGRPVGYVTNIINGLECGRGDGRVADRIGF 297

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QY 295 YKRYCDLLGVSQGNLDCYNQRP 318
      |||||:|||||:|||||:|||||
Db 298 YKRYCDMLGVSIGANLDCYNQRP 321
      |||||:|||||:|||||:|||||

RESULT 5
S40414
Chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C:Accession: S40414
R:Nishizawa, Y.
submitted to the EMBL Data Library, November 1990
A:Reference number: S40414
A:Accession: S40414
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-340 <NIS>
A:Cross-references: EMBL:X56787; NID:g407471; PID:CA40107.1; PID:g407472
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:92-330/Domain: plant chitinase homology <PCH>

Query Match 74.6%; Score 1317.5; DB 2; Length 340;
Best Local Similarity 72.4%; Pred. No. 1e-90;
Matches 228; Conservative 36; Mismatches 50; Indels 1; Gaps 1;

QY 4 VVAVMLAAFAVSAHAECGQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSCNGCS 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 16 LVAVLAAALATAARAECGAGAGARCPNCLCCSRWCGTTSDFCGDGCGQSCGCG- 74

QY 64 GTFVPVPTPSGGVSSIIISQSLFDQMLLRNDACLAAGFYNYGAFVAAANSFSGFATT 123
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 GTPTPTPSDPSDGVGSIVPRDLFERLLLRNDGACPARGFYTFEAFVAAAFPAFGGT 134

QY 124 GSTDVKKREVAFLAQTSHETGGWPTAPDGPYSWCYCNQERGATSDYCTPSSQWPCAP 183
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 GNTETKREVAFLGQTSHTTGGWPTADGPFWSWYCFKQGNPPSDYCPSPENPCAP 194

QY 184 GKRYGGRGPIQIASHNYNYPAGQAIGTDLINPDVLASDATVSFKTALWFWMPQSPKPS 243
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 GRKYGRGPIQLSFNFNYGPAGRAIGVDLLSNPDVLATDVTSFKTALWFWMPQGNKPS 254

QY 244 SHDVTGRWSPSGADAAGRPVGYVITNINGLGECRGQDGRVADRIGFYKRYCDLLG 303
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 255 SHDVTGRWAPSPADAAGRAPGYVITNIVNGLECGHGPDDRVANRIGFYQRYCGAFG 314

QY 304 VSYGDNLDYCNQRP 318
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 315 IGUGNLDYCNQRP 329

RESULT 6
S39979
Chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S39979
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice ch
A:Reference number: S39979; MUID:94049667
A:Accession: S39979
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <NIS>
A:Cross-references: EMBL:X56787
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
```

F:91-329/Domain: plant chitinase homology <PCH>

```
Query Match 74.4%; Score 1313; DB 2; Length 339;
Best Local Similarity 72.9%; Pred. No. 2.2e-90;
Matches 229; Conservative 36; Mismatches 47; Indels 2; Gaps 2;

QY 5 VVAVMLAAFAVSAHAECGQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSCNGCSG 64
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 17 VALAVLAAALATAARAECGAGARCPNCLCCSRWCGTTSDFCGDGCGQSCGCGP 76

QY 65 GTFVPVPTPSGGVSSIIISQSLFDQMLLRNDACLAAGFYNYGAFVAAANSFSGFATTG 124
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 TTPTP-PSPS-DGVGSIVPRDLFERLLLRNDGACPARGFYTFEAFVAAAFPAFGGTG 134

QY 125 STDVKKREVAFLAQTSHETGGWPTAPDGPYSWCYCNQERGATSDYCTPSSQWPCAPG 184
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 NFETKREVAFLGQTSHTTGGWPTADGPFWSWYCFKQGNPPSDYCPSPENPCAPG 194

QY 185 KRYGGRGPIQIASHNYNYPAGQAIGTDLINPDVLASDATVSFKTALWFWMPQSPKPS 244
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 RXYGGRGPIQLSFNFNYGPAGRAIGVDLLSNPDVLATDVTSFKTALWFWMPQGNKPS 254

QY 245 HDVTGRWSPSGADAAGRPVGYVITNINGLGECRGQDGRVADRIGFYKRYCDLLGV 304
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 255 HDVTGRWAPSPADAAGRAPGYVITNIVNGLECGHGPDDRVANRIGFYQRYCGAFGI 314

QY 305 SYGDNLDYCNQRP 318
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 315 GUGNLDYCNQRP 328

RESULT 7
S15997
Chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S15997
R:Zhu, Q.; Lamb, C.J.
Mol. Gen. Genet. 226, 289-296, 1991
A:Title: Isolation and characterization of a rice gene encoding a basic chitinase.
A:Reference number: S15997; MUID:91238706
A:Accession: S15997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <MOL>
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:22-63/Domain: hevein chitin-binding domain homology <HCB>
F:81-320/Domain: plant chitinase homology <PCH>
```

```
Query Match 73.7%; Score 1301.5; DB 2; Length 336;
Best Local Similarity 72.3%; Pred. No. 1.5e-89;
Matches 237; Conservative 27; Mismatches 47; Indels 17; Gaps 4;

QY 1 MRGVVVVYVMLAAAF-AVSAHAECGQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSC 59
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MRALAVVAVYVYVMLAAAFVAAVHAECGQAGGAVCPNCLCCSKFGFCGTTSDYCGAGCQSC 60

QY 60 N-----GCSGTGPVPTPSGGVSSIIISQSLFDQMLLRNDACLAAGFYNYGAFVA 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SRLRRRPDASGG-----GGSGVASIVSRSLFDQMLLRNDACLAAGFYNYGAFVA 112

QY 113 AANSFSGFATTGSDVKKREVAFLAQTSHETGGWPTADGPFWSWYCFNQEER-GAITS 171
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 113 AASAFPFGAAGADATNKRVAFLAQTSHETGGWATADGPFYTWGYCFKEENGAGPD 172

QY 172 YCTPSSQWPCAPGKKYFGRGPIQIASHNYNYPAGQAIGTDLINPDVLASDATVSFTAL 231
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 YCQQAQWPCAAGKKYFGRGPIQLSFNFNYGPAGQAIGADLLGDPDLVASDATVSFTAF 232

QY 232 WFWMTPOSPPSSHDVTGRWSPSGADAAGRPVGYVITNINGLGECRGQDGRVADR 291
```


Db	233	WFWMTQSPKPSCNVATQQTWPSADDRAGRVPGYVNTINGLEGCHGEDDRIADR	292
QY	292	IGFYRYCDLLGVSYGDNLDYINQRPFA	319
Db	293	IGFYRYCDILGVSYGANIDCYSORPSA	320

RESULT 8
T04484
probable chitinase (EC 3.2.1.14) - barley
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T04484
R:Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Plant J. 6, 579-589, 1994
A:Title: Identification of an enhancer/silencer sequence directing the aleurone-specific
A:Reference number: Z15373; MOID:95078949
A:Accession: T04484
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-332 <LEA>
A:Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961
C:Genetics:

C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinases.
A; Gene: CHI33
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinases.
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 28-69/Domain: hevein chitin-binding domain homology <HCB>
F; 85-322/Domain: plant chitinase homology <PCH>

Query Match	73.2%	Score 1291.5;	DB 2;	Length 332;
Best Local Similarity	71.6%;	Pred. No. 8.4e-89;		
Matches 235.	Conservative	33;	Mismatches 43;	Indels 17;
				Gaps 6;

Q7

1 MRG-----VVVVLAAAFVASIAHAEQCGSQAGGATCPNCLCCSXFPGFCGTSDYCGT 53
||| | : | : | : ||||||||| : | : | : |||

D6

1 MEGDSVVVA TIVT SAATAMAVTVZACGCSQAGGATCPNCLCCSRGVCGSTDYCGA 60

Qy 54 GCQSQCGSCGGTPVPVTPSGGGVSSIISQSLFDQMLHRN---DAACLAAGFYNYGAF 110

DB	61	GCQSCSGC-GPTP-PCPSP-GGGVSSIISRDLEFQFLHRDRCDA-----GPTYDAF	170
OY	111	VAAANSFSGFATGTGSTDYKKREVAALFAIOTSHTETIGSWPTAPDGPYSWGYCFNORGATS	170

Db 114 LAAATFPAGTGTSTETRKQVAAFFGQTSHEITGGWATAPDGYSWGVCYRRELGSPP 173

QY	171	DYCTPSSOWPCAPGKKYFGRGP	IQILSHSNYGFAGQAIGTDLNNPD	LNVASDAIVSFRIA	233
		::: :	:	:	
d _b	174	DYCQPSSOWPCVQDRQYYGRGP	PIMLSWNNYGPAGRAIGVDLNNPD	LNVATVSFRFA	233

[illegible]

```

QY      291  RIGFYKRYCDLLGVSYGDNLDYCYNQPF 318
          |||||:||||:||||:||||:||||:||||:

```

1000

chitinase (EC 3.2.1.14) - rice
Sl4948
N:Alternate names: class I endochitinase

```
C;Species: Criza savana (fasc)  
C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999  
C;Accession: S14948
```

Plant Mol. Biol. 16, 479-480, 1991
 A:Title: Nucleotide sequence of a rice genomic clone that encodes a class I endochitinase
 A:Reference number: S14948-MUID:91370895

A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-318 <HUA>
A:Cross-references: EMBL:X54367; NTD:g20195; PIDN:CRA38249.1; PID:g20196
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:19-60/Domain: hevein chitin-binding domain homology <HCB>
F:79-316/Domain: plant chitinase homology <PCH>

	Query Match	73.1%	Score 1289.5;	DB 2;	Length 318;				
	Best Local Similarity	73.4%;	Pred. No. i.i.e-88;						
	Matches 234; Conservative	24;	Mismatches 56;	Indels	5;	Gaps	4;		
Qy	1	MRGVVVVAMLAFAAFVAHAECGSGAAGATPCNLCCKSFEGCGTSTDCYGCQCQQCN	60						
	:	:::	: :	:	:	:	:	:	:
Dd	1	MRALAVVMAMVAV--RGECCGSAGGALCNCCLCSQYSWCGSTSDCYGACQSQCS	58						
	:	:	:	:	:	:	:	:	:
Qy	61	GCSCGTVPVPPSPGGVGSSIISQLFDOMLHRNDAACLAKEYNTGAFVAANSSFGF	120						
	:	:	:	:	:	:	:	:	:
Dd	59	GCSCGTPPSPGGGSGVASIIISPFLDMLLRNQACRAKFYTYYDAFVAANAYPDF	118						
	:	:	:	:	:	:	:	:	:
Qy	121	ATTGSTDVKKREVAFLAQTSHTTCGWPTAPDPGPSWGVCENOE-RGATSDDTYCTPSQW	179						
	:	:	:	:	:	:	:	:	:
Dd	1-9	ATTRDADTCRKREVAFLAQTSHTTCGWPTAPDPGPSWGVCFKREENNGNAFTCEKPEPW	178						
	:	:	:	:	:	:	:	:	:

[illegible]

DB 237 PKPSCHAVITGQWTSADDDQAAGRPVGYGEITNINGVECGHGADKKVADRIGFKRYC 296

QV 300 DLLGVSYGDNLDCYNQRPF 318

Db 297 DMLGSYGDLDCYNQRPY 315

S08627
chitinase (EC 3.2.1.14) precursor - common tobacco
(*Nicotiana glauca* L.)

C.Accession: S08627; JQ0993
C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 22-Jun-1993
R.Shinshi, H.; Neuhaus, J.M.; Ryals, J.; Meins Jr., F.

A:Title: Structure of a tobacco endochitinase gene: evidence that different chitinase
A:Reference number: S08627; MCID:91345623
A:Accession: S08627

A:Molecule type: DNA
A:Residues: 1-329 <SHI>
A:Cross-references: EMBL:X16938; NID:g19860; PDB:CAA34812.1; PDB:g19861

R. Neale, A. D.; Wahleithner, J. A.; Lund, M.; Bonnett, H. T.; Kelly, A.; Meeks-Wagner, D. Plant Cell 2, 673-684, 1990

A:Accession: JQ0993
A:Reference number: JQ0993; MWID:92404740
A:Molecule type: mRNA

A; Cross-references: GB: S44869; NID: g756132; PIDN: AAB23374.1; PID: g756133
A; Experimental source: thin cell layer, cv. samsun nn

C:Genetics:
A; Introns: 148/1; 199/2
C_Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;

F; 7-23/Domain: signal sequence #status predicted <SIG>
F; 24-329/Product: chitinase #status predicted <MAT>

F;83-321/Domain: plant chitinase homology <PCH>

A:Residues: 1-324 <MEI>
A:Cross-references: EMBL:X64519; NID:g19846; PIDN:CAA45822.1; PID:g19847
A:Experimental source: cv. Havana 425
R:Shinshi, H.; Mohnen, D.; Melins Jr., F.
Proc. Natl. Acad. Sci. U.S.A. 84, 89-93, 1987
A:Title: Regulation of a plant pathogenesis-related enzyme: inhibition of chitinase and
A:Reference number: A29074
A:Accession: A29074
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 15-324 <SHI>
R:Fukuda, Y.; Ohme, M.; Shinshi, H.
Plant Mol. Biol. 16, 1-10, 1991
A:Title: Gene structure and expression of a tobacco endochitinase gene in suspension-cul
A:Reference number: S13322; MUID:91363829
A:Accession: S13322
A:Molecule type: DNA
A:Residues: 1-324 <FOK>
A:Cross-references: EMBL:X51599; NID:g19844; PIDN:CAA35945.1; PID:g19845
A:Experimental source: cv. BY4
C:Genetics:
A:Introns: 143/1; 194/2
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-324/Product: chitinase B #status predicted <MAT>
F:24-66/Domain: hevein chitin-binding domain homology <HCB>
F:76-316/Domain: plant chitinase homology <PCH>

Query Match 71.4%; Score 1261; DB 2; Length 324;
Best Local Similarity 72.1%; Pred. No. 1.5e-86;
Matches 225; Conservative 29; Mismatches 50; Indels 8; Gaps 3;

QY 8 AMIAAFAVSAHAEQCSQAGATCPNCLCCSKFGCGTTSDYCGTG-COSQCNCGSGGT 66
Db 11 SLLFSLLSASACQCSQAGARACSLCCSKFGCGTNDYCGPNCQSQCPG--GPT 68
QY 67 PVVPTPSGGVSSITISQSLFDQMLLHRNDAAKLAGFYNYGAFVAANSPSGFATTGST 126
Db 11 SLLFSLLSASACQCSQAGARACSLCCSKFGCGTNDYCGPNCQSQCPG--GPT 68
QY 69 P-----PGGDLGSISSSMFDQMLKHRNDNACQCGKGFYSYNAFINAARSPFGTSGDT 123
QY 127 DVKKREVAFLAQTSHETTGWPTAPDGPYSGWYCFNQRGATSDYCTPSSQWPCAPGK 186
Db 124 TARKREIAAFAQTSHETTGWPTAPDGPYAWGYCFLREQSPGDYCTPSSQWPCAPGK 183
QY 187 YFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSKFTALFWMTPOSPPSSHD 246
Db 184 YFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSKFTALFWMTPOSPPSSHD 243
QY 247 VITGRWSPSGADQAGRPVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGVSY 306
Db 244 VITGRWSPSGADQAGRPVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGVSY 303
QY 307 GDNLDYCNORPF 318
Db 304 GDNLDYCNORPF 315

RESULT 14
S65019
chitinase (EC 3.2.1.14) precursor (clone ChtB1) - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C:Accession: S65019
R:Beerhues, L.; Kombrink, E.
Plant Mol. Biol. 24, 353-367, 1994
A:Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-beta
A:Reference number: S43317; MUID:94154255
A:Accession: S65019
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-318 <BEE>

Query Match 70.8%; Score 1250.5; DB 2; Length 318;
Best Local Similarity 71.6%; Pred. No. 8.9e-86;
Matches 227; Conservative 29; Mismatches 46; Indels 15; Gaps 5;

A:Cross-references: EMBL:U02605; NID:g467819; PIDN:AAA18332.1; PID:g467820
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase
F:19-61/Domain: hevein chitin-binding domain homology <HCB>
F:71-310/Domain: plant chitinase homology <PCH>

Query Match 71.1%; Score 1255.5; DB 2; Length 318;
Best Local Similarity 72.6%; Pred. No. 3.8e-86;
Matches 228; Conservative 26; Mismatches 45; Indels 15; Gaps 5;

QY 9 MIAAFAVSAHAEQCSQAGATCPNCLCCSKFGCGTTSDYCGTG-COSQCNCGSGGTP 67
Db 7 LLLFSLLSASACQCSQAGALCASLCCSKFGCGTNDYCGPNCQSQCPG----- 60
QY 68 VPVPTPSG--GGVSSIIISQSLFDQMLLHRNDAAKLAG--FYNYGAFVAANSPSGFATTG 124
Db 61 --GGPSPGDLGGV--ISNSMFDQMLNHRNDNACQCGKGFYSYNAFINAAGSPFGTGTG 115
QY 125 STDVKKREVAFLAQTSHETTGWPTAPDGPYSGWYCFNQRGATSDYCTPSSQWPCAPG 184
Db 116 DITARKREIAAFAQTSHETTGWPTAPDGPYAWGYCFLREQSPGDYCTPSSQWPCAPG 175
QY 185 KKYFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSKFTALFWMTPOSPPSS 244
Db 176 KKYFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSKFTALFWMTPOSPPSS 235
QY 245 HDVITGRWSPSGADQAGRPVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGV 304
Db 236 HDVITGRWSPSGADQAGRPVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGV 295
QY 305 SYGNDLCYNORPF 318
Db 296 SPGNDLCGNORSF 309

RESULT 15
S43317
chitinase (EC 3.2.1.14) class I precursor (clone ChtB3) - potato (fragment)
N:Alternate names: basic chitinase precursor
C:Species: Solanum tuberosum (potato)
C:Date: 20-Oct-1994 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
C:Accession: S43317; S06161
R:Beerhues, L.; Kombrink, E.
Plant Mol. Biol. 24, 353-367, 1994
A:Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-b
A:Reference number: S43317; MUID:94154255
A:Accession: S43317
A:Molecule type: mRNA
A:Residues: 1-318 <BEE>
A:Cross-references: EMBL:U02607; NID:g467823; PIDN:AAA17409.1; PID:g467824
R:Laflamme, D.; Roxby, R.
Plant Mol. Biol. 13, 249-250, 1989
A:Title: Isolation and nucleotide sequence of cDNA clones encoding potato chitinase g
A:Reference number: S06161; MUID:92003671
A:Accession: S06161
A:Molecule type: mRNA
A:Residues: 3-17, 'GSNVVHRRP', 28-234, 'X', 236-318 <LAF>
A:Cross-references: EMBL:X14133; NID:g21464; PIDN:CAA32351.1; PID:g21465
A:Note: the authors translated the codon CAG for residues 54 and 303 as Gly, YGC for
Y
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F:19-311/Product: chitinase #status predicted <MAT>
F:19-61/Domain: hevein chitin-binding domain homology <HCB>
F:71-310/Domain: plant chitinase homology <PCH>
F:312-318/Domain: carboxyl-terminal propeptide #status predicted <PRO>

```
Qy 6 VVAMLAFAVSAHAEOCSQAGATCPNCLCCSKFCGCTTSDYCGTG-CQSQCNCSG 64
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
4 IFSLLFSLLLINASAEQCSQAGALCAPLCCSKFQWCGNTINDYCGPNCQSQCPG-- 60
Qy 65 GTPVPVPTPSG--GGVSSIIISQSLFDQMLLHRNDAACLAKE-GEYNYGAFVAAAANSFSGFA 121
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
61 -----GCPSPGDLGGV--ISNSMFDQMLNHRNDAACQGNFYNAFISAAGSFPFG 112
Qy 122 TTGSTDVKKREVAFLAQTSHETTGWFTAPDGPYSWGYPNQERGAATSDYCTPSSQWPC 181
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
113 TTGDITARKREIAAFLAQTSHETTGWPSAPDGPYAWGYCFLREQSGPDYCTPSSQWPC 172
Qy 182 APGRKYFCRGPQIOLSHNNYKGPAGQAIGTDLNNPDLVADATVSFKTALWFWMTPOS PK 241
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
173 APGRKYFCRGPQIOLSHNNYKGPAGQAIGTDLNNPDLVADATVSFKTALWFWMTPOS PK 232
Qy 242 PSSHDVITGRWSPSGADQAGRVFGYGYITNIINGGLECGRQDGRVADRIGFYKRYCDL 301
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
233 PSCHDVITGRWQPSGADQAGRVFGYGYITNIINGGLECGHGSRSRQDRIGFYKRYCGI 292
Qy 302 LGVSYGDNLDYCNORPF 318
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
293 LGVSYGDNLDYCNORSE 309
```

Search completed: May 3, 2002, 18:32:13
Job time: 7476 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:48:32 ; Search time 78.59 seconds
(without alignments)
148.824 Million cell updates/sec

Title: US-09-534-229c-3

Perfect score: 1765

Sequence: 1 MRGVVVVMAAAFAVSAHA.....DLGVSYGNDLCYNQRPFA 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1407.5	79.7	318	1 CH11_HORVU	P11955 hordeum vul
2	1301.5	73.7	336	1 CH12_ORYSA	P25765 oryza sativ
3	1289.5	73.1	318	1 CH11_ORYSA	P24626 oryza sativ
4	1281.5	72.6	329	1 CH11_TOBAC	P08252 nicotiana t
5	1261.5	71.4	324	1 CH12_TOBAC	P24091 nicotiana t
6	1255.5	71.1	318	1 CH11_SOLTU	P52403 solanum tub
7	1250.5	70.8	318	1 CH13_SOLTU	P52405 solanum tub
8	1248.5	70.7	322	1 CH13_LYCES	Q05538 lycopersico
9	1240.5	70.3	316	1 CH12_SOLTU	P52404 solanum tub
10	1215.5	68.8	320	1 CH12_PEA	P36907 pisum sativ
11	1208.5	68.4	324	1 CH12_PEA	P21226 pisum sativ
12	1208.5	68.4	328	1 CH12_SOLTU	P05315 solanum tub
13	1206.5	68.3	334	1 CH13_TOBAC	P29059 nicotiana t
14	1193.5	67.6	302	1 CH14_SOLTU	P52406 solanum tub
15	1192.5	67.6	322	1 CH12_BRANA	Q09023 brassica na
16	1190.5	67.5	322	1 CH1T_ARATH	P19171 arabidopsis
17	1187.5	67.3	314	1 CH1B_VITVI	P51613 vitis vinif
18	1183.5	67.0	328	1 CH1T_PHAVU	P06215 phaseolus v
19	1178.5	66.8	324	1 CH11_GOSHI	Q39799 gossypium h
20	1168.5	66.2	327	1 CH15_PHAVU	P36361 phaseolus v
21	1154.5	65.4	302	1 CH12_GOSHI	Q39785 gossypium h
22	1151.5	65.2	321	1 CH11_THECC	Q41596 theobroma c
23	1125.5	63.7	266	1 CH12_HORVU	P23951 hordeum vul
24	1022.5	57.9	340	1 CH16_POPTR	P16579 populus tri
25	1004.5	56.9	246	1 CH1D_LYCES	Q05537 lycopersico
26	874.5	49.5	303	1 CH1B_POPTR	P29031 populus tri
27	805.5	45.6	254	1 CH1T_PETHY	P29021 petunia hyb
28	803.5	45.5	316	1 CH18_POPTR	P16061 populus tri
29	791.5	44.8	247	1 CH1B_LYCES	Q05540 lycopersico
30	785.5	44.5	253	1 CH1Q_TOBAC	P17514 nicotiana t
31	763.5	43.3	253	1 CH1P_TOBAC	P17513 nicotiana t
32	722.5	40.9	372	1 AG1_URTDI	P11218 urtica dioi
33	712.5	40.4	253	1 CH1A_LYCCI	Q40114 lycopersico

RESULT 1

ID	CH11_HORVU	STANDARD;	PRT;	318 AA.
AC	P11955;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	26 KDA ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=4513;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. NK 1558; TISSUE=Leaf;			
RA	Ignatius S.M.J.; Huang J.; Muthukrishnan S.;			
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.			
RL	[2]			
RP	SEQUENCE OF 141-318 FROM N.A.			
RC	STRA=N-CV. HIMALAYA;			
RA	Swiegie M.; Huang J.-K.; Lee G.; Muthukrishnan S.;			
RT	"Identification of an endochitinase cDNA clone from barley aleurone cells."			
RL	Plant Mol. Biol. 12:403-412(1989).			
CC	-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN			
CC	-!- CONTAINING FUNGAL PATHOGENS.			
CC	-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF			
CC	N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.			
CC	-!- INDUCTION: BY ETHYLENE.			
CC	-!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO			
CC	CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL			
CC	CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL			
CC	HYDROLASES).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
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CC	-----			
CC	EMBL: U02287; AAA18586.1; -			
DR	EMBL: X15349; CAA33407.1; -			
DR	PIR: S04131; S04131.			
DR	HSSP: P23951; 2BAA.			
DR	InterPro: IPR001002; Chitin_bind.			
DR	InterPro: IPR000726; Glyco_hydro_19.			
DR	Pfam: PF00187; chitin_binding; 1.			
DR	Pfam: PF00182; Glyco_hydro_19; 1.			
DR	PRINTS: PR00451; CHITINBINDING.			
DR	ProDom: PD000574; Glyco_hydro_19; 1.			
DR	ProDom: PD000609; Chitin_bind; 1.			
DR	SMART: SM00270; ChitBD1; 1.			
DR	PROSITE; PS00773; CHITINASE_19_1; 1.			

ALIGNMENTS

34	692.5	39.2	253	1	CH1A_LYCES
35	609.5	34.5	288	1	CHIP_BETVU
36	599.5	34.0	269	1	CHIP_MAIZE
37	579	32.8	268	1	CH14_BRANA
38	577	32.7	280	1	CH1A_MAIZE
39	547	31.0	270	1	CH14_PHAVU
40	503	28.5	250	1	CHIT_DIOJA
41	297	16.8	121	1	CHIC_POPTR
42	285.5	16.2	133	1	IAMY_COILA
43	208	11.8	46	1	CH13_ARAHY
44	205	11.6	212	1	AG1_HORVU
45	201	11.4	45	1	CH1A_ARAHY

Q05539	lycopersico
P42820	beta vulgar
P29023	zea mays (m
Q06209	brassica na
P29022	zea mays (m
P27054	phaseolus v
P80052	dioscorea j
P29032	populus tri
P15326	colx lachry
Q06015	arachis hyp
P15312	hordeum vul
Q06012	arachis hyp


```

RL Plant Mol. Biol. 16:479-480(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC -----
CC EMBL; X54367; CAA38249.1; -.
CC DR PIR; S14948; S14948.
CC DR HSSP; P02877; IHEV.
CC DR InterPro; IPR001002; Chitin_bind.
CC DR InterPro; IPR000726; Glyco_hydro_19.
CC DR Pfam; PF00187; chitin_binding; 1.
CC DR PRINTS; PR00451; CHITINBINDNG.
CC DR ProDom; PD000574; Glyco_hydro_19; 1.
CC DR ProDom; PD000609; Chitin_bind; 1.
CC DR SMART; SM00270; ChitBD1; 1.
CC DR PROSITE; PS00026; CHITIN_BINDING; 1.
CC DR PROSITE; PS00773; CHITINASE_19_1; 1.
CC DR PROSITE; PS00774; CHITINASE_19_2; 1.
CC DR Multibase family.
CC KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 318 BASIC ENDOCHITINASE 1.
FT DOMAIN 19 61 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 21 36 BY SIMILARITY.
FT DISULFID 30 42 BY SIMILARITY.
FT DISULFID 35 49 BY SIMILARITY.
FT DISULFID 53 57 BY SIMILARITY.
SQ SEQUENCE 318 AA; 33695 MW; 8FD37913450CC7EB CRC64;

Query Match 73.1%; Score 1289.5; DB 1; Length 318;
Best Local Similarity 73.4%; Pred. NO. 5.7e-90;
Matches 234; Conservative 24; Mismatches 56; Indels 5; Gaps 4;

QY 1 MRGVVVAIAAFAVSAHAECGSGAGGATCPNCLCCSKFCGCTTSDYCGTGCSQCN 60
DB 1 MRALAVAVMAVAV--RGEQCGSQAGGALCPNCLCCSQYGCWGCTSDYCGAGCQSCS 58
QY 61 GCGSGTVPVPPFSGGSGVSIISLFDQMLLRNDAACLRKGFYNYGAFVAAANSFSGF 120
DB 59 GCGCGGPPFSGGSGVSIISLFDQMLLRNDAACLRKGFYDYFAVAAANAYPDF 118
QY 121 ATGTSTDKKREVAFLAQTSHETTGWPTADGPGYSWGYCENQE--RGATSDYCTPSSQW 179
DB 119 ATTRDADTKREVAFLAQTSHETTGWPTADGPGYSWGYCENQNPATYCEFKPEW 178
QY 180 PCAPGKKEFGPIQISHNYNYPGPAQATGTDLNNPDLVADATVSEKTLKFWMTPOS 239
DB 179 PCAARKKYYGRPIQITYINYNG--RGAGTGSLLNPNPDLVADSA--VSFKTAFWFWMTPOS 236
QY 240 KPPSSHDVITGRWSPGADQAAGRVPGYVITNINIGGLECGRGQDGRVADRIGFYKRYC 299
DB 237 KPPSCHAVITGQWTPSADQAAGRVPGYGEITNININGVECGHGADDKVADRIGFYKRYC 296
QY 300 DLGVSYGDNLCYNQRP 318
DB 297 DMLGVSYGDNLCYNQRP 315

```

```

RESULT 4
CHIL_TOBAC
ID CHIL_TOBAC STANDARD; PRT; 329 AA.
AC P08252;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
GN CHN48.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAVANA 425; TISSUE=Leaf;
RX MEDLINE=51346623; PubMed=1966383;
RA Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr.;
RT "Structure of a tobacco endochitinase gene: evidence that different
RT chitinase genes can arise by transposition of sequences encoding a
RT cysteine-rich domain.";
RL Plant Mol. Biol. 14:357-368(1990).
RN [2]
RP SUBCELLULAR LOCATION.
RX MEDLINE=32052270; PubMed=1946457;
RA Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
RT "A short C-terminal sequence is necessary and sufficient for the
RT targeting of chitinases to the plant vacuole.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
RN [3]
RP HYDROXYLATION.
RX MEDLINE=92358209; PubMed=1496378;
RA Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.;
RT "Vacuolar chitinases of tobacco: a new class of hydroxyproline-
RT containing proteins.";
RL Science 257:655-657(1992).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -!- INDUCTION: BY ETHYLENE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16938; CAA34812.1; -.
CC DR EMBL; X16939; CAA34813.1; -.
CC DR PIR; S08627; S08627.
CC DR HSSP; P23951; 2BAA.
CC DR InterPro; IPR001002; Chitin_bind.
CC DR InterPro; IPR000726; Glyco_hydro_19.
CC DR Pfam; PF00187; chitin_binding; 1.
CC DR Pfam; PF00182; Glyco_hydro_19; 1.
CC DR PRINTS; PR00451; CHITINBINDNG.
CC DR ProDom; PD000574; Glyco_hydro_19; 1.
CC DR ProDom; PD000609; Chitin_bind; 1.
CC DR SMART; SM00270; ChitBD1; 1.
CC DR PROSITE; PS00026; CHITIN_BINDING; 1.
CC DR PROSITE; PS00773; CHITINASE_19_1; 1.
CC DR PROSITE; PS00774; CHITINASE_19_2; 1.
CC KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Hydroxylation; Multigene family.

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FT SIGNAL 1 23
FT CHAIN 24 322
FT PROPEP 323 329
FT DOMAIN 24 65
FT DISULFID 26 41
FT DISULFID 35 47
FT DISULFID 40 54
FT DISULFID 59 63
FT MOD_RES 67 67
FT MOD_RES 69 69
FT MOD_RES 71 71
FT MOD_RES 72 72
FT MOD_RES 74 74
FT MOD_RES 75 75
FT SEQUENCE 329 AA; 35156 MW; 3EC99D96E6C0114C CRC64;

Query Match 72.6%; Score 1281.5; DB 1; Length 329;
Best Local Similarity 73.2%; Pred. No. 2.4e-89;
Matches 229; Conservative 29; Mismatches 50; Indels 5; Gaps 4;

QY 8 AMLAAAFNYSAAHAEQGSQAGGATCNCLCCSKFGCGTSDXCGTG-COSQCNCGSGGT 66
Db 11 SLIFSULLLSASAEQGSQAGGARGCPSCGLCCSKFGCGTNDYCGPNCOSQCPG--GPT 68
QY 67 PVPVPTPSGGG-VSSIISOSLFDQMLLHRNDAACLAKGFNYGAFVAAANFSFGFATGGS 125
Db 69 PTP-PTPPGGDLGSISSSMFDMKLKRNDAACQKGFVYNFAFINAARSFFGFGTSGD 127
QY 126 TDVKKREVAFTAQTHETGGHTPADPGYSWGYCFNBERGATSDYCPSSQWPCAPGK 185
Db 128 TARKREIAFAAQTSHETGGWATPDGPGYAWGYCWLREQSPGDYCTPSGQWPCAPGR 187
QY 186 KYFGRGPQIOTSHNRYGPAQOATGTDLLNPNPLVADATVSEKTLFWMTFMTPOSPKPSH 245
Db 188 KYFGRGPQIHSNRYNGPCGARGVLLNPNPLVADDPVLSFKSALFWMTPOSPKPSCH 247
QY 246 DVTIGRWSPGADQAGRVPGYGVININGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
Db 248 DVTIGRWSPGADQAGRVPGYGVININGLECGRGQDGRVADRIGFYKRYCDLLGVS 307
QY 306 YGDNLCYNQRPF 318
Db 308 PGDNLCGNQRF 320

RESULT 5
CHI2_TOBAC STANDARD; PRT; 324 AA.
AC P24091;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (CHN-B).
GN CHN50.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BRIGHT YELLOW 4; TISSUE=Leaf;
RX MEDLINE=91363829; PubMed=188889;
RA Fukuda Y., Ohme M., Shinshi H.;
RT "Gene structure and expression of a tobacco endochitinase gene in
RL suspension-cultured tobacco cells.";
RN Plant Mol. Biol. 16:1-10(1991).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAVANA 425; TISSUE=Leaf;
RX MEDLINE=92269767; PubMed=1588915;
RA van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.;

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RT "The structure and regulation of homeologous tobacco endochitinase
genes of Nicotiana sylvestris and N. tomentosiformis origin.";
RL Mol. Gen. Genet. 232:460-469(1992).
RN [3]
RN SEQUENCE OF 15-324 FROM N.A., AND SEQUENCE OF 24-53.
RC STRAIN=CV. HAVANA;
RA Shinshi H., Mohnen D., Meins F. Jr.;
RT "Regulation of a plant pathogenesis-related enzyme: inhibition of
chitinase and chitinase mRNA accumulation in cultured tobacco tissues
by auxin and cytokinin.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:89-93(1987).
RN [14]
RN SUBCELLULAR LOCATION.
RX MEDLINE=92052270; PubMed=1946457;
RA Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
RT "A short C-terminal sequence is necessary and sufficient for the
targeting of chitinases to the plant vacuole.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
RN [15]
RN HYDROXYLATION.
RX MEDLINE=92358209; PubMed=1496378;
RA Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.;
RT "Vacuolar chitinases of tobacco: a new class of hydroxyproline-
containing proteins.";
RL Science 257:655-657(1992).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF CHITIN.
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -!- INDUCTION: BY ETHYLENE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDES A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
CC -----
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CC -----
CC EMBL; X51599; CAA35945.1; -.
CC EMBL; X64519; CAA45822.1; -.
CC EMBL; M15173; AAA34070.1; -.
CC PIR; A29074; A29074.
CC PIR; S13322; S13322.
CC PIR; S20981; S20981.
CC HSSP; P23951; ZBAA.
CC InterPro; IPR001002; Chitin_bind.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00187; chitin_binding; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC PRINTS; PR00451; CHITINBINDNG.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC ProDom; PD000609; Chitin_bind; 1.
CC SMART; SM00270; ChtBD1; 1.
CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
CC Hydrolase; glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Hydroxylation; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 317 ENDOCHITINASE B.
FT PROPEP 318 324 REMOVED IN MATURE FORM (PROBABLE).
FT DOMAIN 24 65 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION.

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FT MOD_RES 69 69 HYDROXYLATION.
SQ SEQUENCE 324 AA; 34721 MW; FA65DC2113B33EB6 CRC64;

Query Match 71.4%; Score 1261; DB 1; Length 324;
Best Local Similarity 72.1%; Pred. No. 8e-88;
Matches 225; Conservative 29; Mismatches 50; Indels 8; Gaps 3;

QY 8 AMLAAAFVSAHAEQCGAGATPCNLCCKSKFGCTGTTSDYCGTG-CQSQCNCGSGGT 66
Db 11 SLLSLLLSASAEQCGAGATPCNLCCKSKFGCTGTTSDYCGTG-CQSQCNCGSGGT 68
QY 67 PVPVPTSGGGVSSIIISQSLFDQMLLNHRNDAAKAGFYNYGAFVAAANSFSGFATTG 126
Db 69 P-----PGGGDLGSIISSMFQMLKRNDAACQCKGFSYNAPFINAARSFPFGTSGDT 123
QY 127 DVKKREVAFLAQTSHTTGGWPTAPDGPYSGWYCFNDEGATSDYCTPSSQWPCAPGK 186
Db 124 TARKREIAAFAQTSHETGGWATAPDGPYANGYCWLRQGGSPGDCYTPSGQWPCAPGK 183
QY 167 YFGRGPIQISHNYNGPAGQAIGTDLNNDLVASDATVSFKTALWFMTQSPKPSHD 246
Db 164 YFGRGPIQISHNYNGPAGQAIGTDLNNDLVASDATVSFKTALWFMTQSPKPSHD 243
QY 247 VITGRWSPGDAQAGRPVGYGVITNIINGGLECGRQDGRVADRIGRYKRYCDLLGVSY 306
Db 244 VITGRWSPGDAQAGRPVGYGVITNIINGGLECGRQDGRVADRIGRYKRYCDLLGVSY 303
QY 307 GDNLDYCNORPF 318
Db 304 GDNLDYCNORPF 315

RESULT 6
CH13_SOLUTU STANDARD; PRT; 318 AA.
ID CH13_SOLUTU
AC P52403;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CH13.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=941154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
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CC or send an email to license@isb-sib.ch).
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CC EMBL; U02605; AAA18332.1; -
CC HSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChEBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19; 1; 1.
DR PROSITE; PS00774; CHITINASE_19; 2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT NON_TER 1
FT SIGNAL <1 18
FT CHAIN 19 311
FT PROPEP 312 318
FT
FT DOMAIN 19 60 CHITIN-BINDING (BY SIMILARITY).
FT DISULFD 21 36 BY SIMILARITY.
FT DISULFD 30 42 BY SIMILARITY.
FT DISULFD 35 49 BY SIMILARITY.
FT DISULFD 54 58 BY SIMILARITY.
SQ SEQUENCE 318 AA; 33813 MW; A0B49DA528706AAA CRC64;

Query Match 71.1%; Score 1255.5; DB 1; Length 318;
Best Local Similarity 72.6%; Pred. No. 2e-87;
Matches 228; Conservative 26; Mismatches 45; Indels 15; Gaps 5;

QY 9 MIAAFAVSAHAEQCGAGATPCNLCCKSKFGCTGTTSDYCGTG-CQSQCNCGSGGT 67
Db 7 LLFSVILLLSASAEQCGAGATPCNLCCKSKFGCTGTTSDYCGTG-CQSQCNCGSGGT 60
QY 68 VFPVTPSG--GGVSSIIISQSLFDQMLLNHRNDAAKAG--FYNYGAFVAAANSFSGFATTG 124
Db 61 --GPGPSGLDGV--ISNSMFDQMLNHRNDAAKAG--FYNYGAFVAAANSFSGFATTG 115
QY 125 STDVKKREVAFLAQTSHTTGGWPTAPDGPYSGWYCFNDEGATSDYCTPSSQWPCAPG 184
Db 116 DITARKREIAAFAQTSHETGGWPTAPDGPYANGYCWLRQGGSPGDCYTPSGQWPCAPG 175
QY 185 KYFGRGPIQISHNYNGPAGQAIGTDLNNDLVASDATVSFKTALWFMTQSPKPS 244
Db 176 KYFGRGPIQISHNYNGPAGQAIGTDLNNDLVASDATVSFKTALWFMTQSPKPS 235
QY 245 HDVITGRWSPGDAQAGRPVGYGVITNIINGGLECGRQDGRVADRIGRYKRYCDLLGV 304
Db 236 HDVITGRWSPGDAQAGRPVGYGVITNIINGGLECGRQDGRVADRIGRYKRYCDLLGV 295
QY 305 SYGDNLDYCNORPF 318
Db 296 SPGDNLDYCNORPF 309

RESULT 7
CH13_SOLUTU STANDARD; PRT; 318 AA.
ID CH13_SOLUTU
AC P52405;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CH13.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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FT SIGNAL 1 22
FT CHAIN 23 315
FT PROPER 316 322
FT DOMAIN 23 64
FT DISULFID 25 40
FT DISULFID 34 46
FT DISULFID 39 53
FT DISULFID 58 62
FT MOD_RES 66 66
FT MOD_RES 68 68
SQ SEQUENCE 322 AA; D13A9191AE8BFC5A CRC64;

Query Match 70.7%; Score 1248.5; DB 1; Length 322;
Best Local Similarity 72.6%; Pred. No. 6.9e-87;
Matches 228; Conservative 25; Mismatches 46; Indels 15; Gaps 5;

QY 9 MLAFAFVSAHAECGQAGGATPCNLCCKSGKFGCTTSDYCGTG-CQSCNCGCGGTP 67
Db 11 LLSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGTNEYCGPNCQSQCPG----- 64
QY 68 VVPVTPSG--CGVSSIIISQSLFDQMLHRNDAACLAK-GFVNYGAFVAAANSFSEATTG 124
Db 65 --GPGPSGDLGV---ISNSMEDQMLHRNDNACQKNNEYSYNAFVTAAGSFEGCTG 119
QY 125 STDVKKREVAFLAQTSHETTGWPTADPGPYSWGYCFNQRGATSDYCTPSSQWPCAPG 184
Db 120 DITARKREIAFLAQTSHETTGWPTADPGPYAGWGYCLFREGSPGDTCTPSSQWPCAPG 179
QY 185 KKYGRGPIQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPS 244
Db 180 KKYGRGPIQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPS 239
QY 245 HDVTGKRWSPGDAQAGRVPGVYVNIINGLECGRGQDGRVADRIGFYKRYCDLIGV 304
Db 240 HDVTGKRWSPGDAQAGRVPGVYVNIINGLECGRGQDGRVADRIGFYKRYCDLIGV 299
QY 305 SYGNLDCYNORPF 318
Db 300 SPGENLDCGNQSRF 313

RESULT 9
CH12_SOLTU STANDARD; PRT; 316 AA.
AC P52404;
DT 01-OCN-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTB2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_taxid=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerrhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
OLD ROOT SEGMENTS, AND CARPELS.

CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
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CC -----
CC EMBL; U02606; AAA17408.1; -.
CC HSP; P23951; 2BAA.
DR InterPro: IPR001002; Chitin_bind.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam: PF00187; chitin_binding; 1.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR ProDom: PD000609; Chitin_bind; 1.
DR SMART: SMO0270; ChtBD1; 1.
DR PROSITE: PS00026; CHITIN_BINDING; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT NON_TER 1
FT SIGNAL <1 18
FT CHAIN 19 309
FT PROPEP 310 316
FT
FT DOMAIN 19 60
FT DISULFID 21 36
FT DISULFID 30 42
FT DISULFID 35 49
FT DISULFID 54 58
SQ SEQUENCE 316 AA; 33629 MW; 81FB3DB3F222A0C6 CRC64;

Query Match 70.3%; Score 1240.5; DB 1; Length 316;
Best Local Similarity 70.8%; Pred. No. 2.7e-86;
Matches 221; Conservative 31; Mismatches 47; Indels 13; Gaps 4;

QY 9 MLAFAFVSAHAECGQAGGATPCNLCCKSGKFGCTTSDYCGTG-CQSCNCGCGGTP 67
Db 7 LLSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGTNEYCGPNCQSQ---CPGSP 63
QY 68 VVPVTPSGGVSSIIISQSLFDQMLHRNDAACLAK-GFVNYGAFVAAANSFSEATTG 126
Db 64 -----GDLGGVISNSMFDQMLHRNDNACQKGNFYSYNAFISAAGSFPFGTTGDI 115
QY 127 DVKKREVAFLAQTSHETTGWPTADPGPYSWGYCFNQRGATSDYCTPSSQWPCAPGK 186
Db 116 TARKREIAFLAQTSHETTGWPTADPGPYAGWGYCLFREGSPGDTCTPSSQWPCAPGRK 175
QY 187 YFGRGPIQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPSHD 246
Db 176 YFGRGPIQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPSHD 235
QY 247 VITGRWSPGDAQAGRVPGVYVNIINGLECGRGQDGRVADRIGFYKRYCDLIGVSY 306
Db 236 VITGRWSPGDAQAGRVPGVYVNIINGLECGRGQDGRVADRIGFYKRYCDLIGVSP 295
QY 307 GDNLDCYNORPF 318
Db 296 GDNLDCGNQSRF 307

RESULT 10
CH1X_PEA STANDARD; PRT; 320 AA.
ID CH1X_PEA


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DR PRINTS; PR00451; CHITINBINDNG.
DR PRODom; PD000574; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtdB1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR HydroLase; Glycosidase; Chitin degradation; Chitin-binding;
KW Multigene family; Signal.
FT SIGNAL 1 20
FT CHAIN 21 309 ENDOCHITINASE A2.
FT PROPEP 310 324 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 21 62 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 55 59 BY SIMILARITY.
SQ SEQUENCE 324 AA; 34678 MW; 540F0DA5EC1D2FA CRC64;

Query Match 68.4%; Score 1208; DB 1; Length 324;
Best Local Similarity 69.0%; Pred. No. 7.6e-84;
Matches 216; Conservative 31; Mismatches 54; Indels 12; Gaps 3;

QY 7 VAMLAARFVVS-AHAEOCGSQAGGATPCNCLCCSKFGCGTTSYCGTCCQSCNCGSG 65
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 IPILLVLVTVCCSACQGTQAGGALCPGGCLCCSKFPGWCGSTSEYCGDGCQSCSGSG- 64
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
66 TPVPYPTSGGVSIIISQSLFDQMLLRNDAACLAAGFYNTGAFVAANSESGFATIGS 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 -----GGTSLISLSDGTENNMLKRNDAACQCKPFTYTDALSAKAAPFNANKGD 115
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 TDVKKREVAFLAQTSHETTGWPTADPGPYSGVCFNQRGATSDYCPSPQWCPAPGK 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 TATKKREIAAFLQGTSHETTGWPTADPGPYAWGCFLEQN-PSYTCQASSEFFCASK 174
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 KYFGRGPTQISNRYNYGPAQGAIGTDLNLPDLVASDATVSEKTLWFWMTQSPKPSH 245
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 QYVYGRGPTQISNRYNYGQCGRAIGVDLLNLPDLVADPVISFKTLWFWMTQSPKPSCH 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 DVIITGRWPSGADAGRGVPGYVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGS 305
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 DVIITGRWPSADRAAGRLPGYGTNTNIINGGLECGRGQDGRVADRIGFYKRYCDIFIG 294
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 YGDNLDYCNQREF 318
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 YGDNLDYCSQREF 307
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
CHIT_SOLTU
ID CHIT_SOLTU STANDARD; PRT; 328 AA.
AC P05315;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RUSSET BURBANK;
RX MEDLINE=89345190; PubMed=2762165;
RA Gaynor J.J., Unkenholz K.M.;
RT "Sequence analysis of a genomic clone encoding an endochitinase from
  Solanum tuberosum.";
RL Nucleic Acids Res. 17:5855-5855(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RUSSET BURBANK;
RX MEDLINE=88262525; PubMed=3387233;
```

```
RA PRINTS; PR00451; CHITINBINDNG.
RT "Primary structure of an endochitinase mRNA from Solanum tuberosum.";
RL Nucleic Acids Res. 16:5210-5210(1988).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- INDUCTION: BY ETHYLENE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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DR EMBL; X07130; CAA30142.1; -.
DR EMBL; X15494; CAA33517.1; -.
DR EIR; S05426; S05426.
DR HSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR00726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR PRODom; PD000574; Glyco_hydro_19; 1.
DR PRODom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtdB1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW HydroLase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 321 ENDOCHITINASE.
FT PROPEP 322 328 REMOVED IN MATURE FORM (PROBABLE).
FT DOMAIN 27 71 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 29 44 BY SIMILARITY.
FT DISULFID 38 50 BY SIMILARITY.
FT DISULFID 43 57 BY SIMILARITY.
FT DISULFID 62 66 BY SIMILARITY.
SQ SEQUENCE 328 AA; 35406 MW; 669B82159BC176EF CRC64;
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Query Match 68.4%; Score 1208; DB 1; Length 328;
Best Local Similarity 69.0%; Pred. No. 7.7e-84;
Matches 218; Conservative 31; Mismatches 57; Indels 10; Gaps 4;

QY 7 VAMLAARFVVS--SAHAEOCGSQAGGATPCNCLCCSKFGCGTTSYCGTG-CQSCNCG 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
10 VAYLFSLVLVLSAALQNCGSGGGKACASGCCSKFCWCGTNDYCGSGNCQSQ---C 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 SGGTPVPVPTPSGGVSSIIISQSLFDQMLLRNDAACLAAGFYNTGAFVAANSESGFAT 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 PGGGPGPGP---GGDLGSAISNMFQMLKRNENSCQCKNFYSYNAFINAARSPPGFT 123
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 TGSTDVKKREVAFLAQTSHETTGWPTADPGPYSGVCFNQRGATSDYCPSPQWCPA 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 SGDINARKEIAAFAAQTSHETTGWASAPDGPYAWGYCFLREGRNPGDYCPSPQWCPA 183
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 PGKPYGGRGPTQISNRYNYGPAQGAIGTDLNLPDLVASDATVSEKTLWFWMTQSPK 242
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
184 PGKPYGGRGPTQISNRYNYGPAQGAIGTDLNLPDLVASDATVSEKTLWFWMTQSPK 243
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 SSHDVTGRWPSGADAGRGVPGYVITNIINGGLECGRGQDGRVADRIGFYKRYCDLL 302
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
244 SCHDVLIGRWNPSSADRAANRLPGYGTNTNIINGGLECGRGQDGRVADRIGFYKRYC 303
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 303 GYSYGNLDYCNORPF 318
DB 304 GVTGPNLDYCNORWF 319

RESULT 13
CHT3_T0BAC
ID CHT3_T0BAC STANDARD; PRT; 334 AA.
AC P29059;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14).
GN CHTN4.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, HAVANA 425; TISSUE=Leaf;
RX MEDLINE=92269767; PubMed=1598915;
RA van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.;
RT "The structure and regulation of homeologous tobacco endochitinase
genes of Nicotiana sylvestris and N. tomentosiformis origin.";
RL Mol. Gen. Genet. 232:460-469(1992).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS (PROBABLE).
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
CC EMBL; X64518; CAA45821.1; -.
CC PIR; S20982; S20982.
CC HSP; P27275; IMMC.
CC InterPro; IPR001002; Chitin_bind.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00187; chitin_binding; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC PRINTS; PR00451; CHITINB_NDNG.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC ProDom; PD000609; Chitin_bind; 1.
CC SMART; SM00270; ChtBD1; 1.
CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC PROSITE; PS00773; CHITINASE_19; 1.
CC PROSITE; PS00774; CHITINASE_19; 2; 1.
CC Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
CC Hydroxylation; Multigene family.
CC SIGNAL
FT CHAIN 1 23
FT PROPEP 24 327 ENDOCHITINASE 3.
FT DOMAIN 328 334 REMOVED IN MATURE FORM (PROBABLE).
FT DISULFID 24 65 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 69 HYDROXYLATION (POTENTIAL).
FT MOD_RES 69 69 HYDROXYLATION (POTENTIAL).
FT SEQUENCE 334 AA; 36220 MW; 4F684CE1FBD432FB CRC64;

Query Match 68.3%; Score 1206; DB 1; Length 334;
Best Local Similarity 67.9%; Pred. No. 1.le-83;
Matches 214; Conservative 32; Mismatches 65; Indels 4; Gaps 2;

QY 8 AMLAAFAVSAHAECGSOAGGATCPNCLCCSKFQFCGTTSDYCYGTG-CQSQCNCGSGGT 66
DB 11 SLILVLELLLAVSAGCGKQAGGARGCPGMCSCNFGWCGNTQDYCGPGKCSQCSPSPGPT 70
QY 67 ---PVPVTPSGGVSSIIISQSLFDQMLLRNDAACLAGFYNYGAFVAAANSFSAFAT 123
DB 71 PRPPTPTGPTGDTISIISSMFDQMLKRNNTQCGKSFYTNAFITAAKSEFGFT 130
QY 124 GSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQERGAITSDYCTSSQWPCAP 183
DB 131 GDTTRKREVAFAAQTSHTTGGWTPADPGYAWGYCYLREGGNPPSYCVSSQWPCAP 190
QY 184 GKRYGGRGPIQISHNNYNGPAGOAIGTDLNPNDLVASDATVSFKTALFWMTWTPSPKPS 243
DB 191 GKRYGGRGPIQISYNNYNGPAGRAIQGLNPNDLVATNAVVSFKSAIWFMTAQSPKPS 250
QY 244 SHDVTGRWSPSGADQAGRVPGYGVITNLINGLGLCGRGDGRVADRIGFYKRYCDLLG 303
DB 251 CHDVTIGRWTPPSAADRANKLPYGVITNLINGLGLCGHSDARVODRIGFYRYCSILG 310
QY 304 VSYGDNLDYCNORPF 318
DB 311 VSPGDNIDCGNOKSF 325

RESULT 14
CHT4_SOLTU
ID CHT4_SOLTU STANDARD; PRT; 302 AA.
AC P52406;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 4 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTB4.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
CC SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
CC SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
CC OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC -----
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QM protein - protein search, using sw model

Run on: May 3, 2002, 18:47:01 ; Search time 157.87 Seconds
(without alignments)
295.565 Million cell updates/sec

Title:
Perfect score: 1765
Sequence: 1 MRGVVVVMAAAFAVSAHA.....DLIGVSYGNDLDCYNQRPFA 319

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL17:*

- 1: sp.archaea:*
 - 2: sp.bacteria:*
 - 3: sp.fungi:*
 - 4: sp.human:*
 - 5: sp.invertebrate:*
 - 6: sp.mammal:*
 - 7: sp.mhc:*
 - 8: sp.organelle:*
 - 9: sp.phage:*
 - 10: sp.plant:*
 - 11: sp.prodent:*
 - 12: sp.virus:*
 - 13: sp.vertebrate:*
 - 14: sp.unclassified:*
- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	1696.5	96.1	Q41539 triticum ae
2	1675.5	94.9	Q9axr9 secale cere
3	1597	90.5	Q9sqli3 poa pratens
4	1557	88.2	Q9sqli4 poa pratens
5	1421	80.5	Q9frv1 secale cere
6	1359.5	77.0	Q42993 oryza sativ
7	1352.5	76.6	Q42994 oryza sativ
8	1317.5	74.6	Q43294 oryza sativ
9	1305	73.9	Q93680 persea amer
10	1291.5	73.2	Q42839 hordeum vul
11	1279	72.5	Q42992 oryza sativ
12	1274	72.2	Q42995 oryza sativ
13	1272.5	72.1	Q40667 oryza sativ
14	1260	71.4	Q41180 nicotiana t
15	1256	71.2	Q9fs45 vitis vinif
16	1253	71.0	Q9few1 nicotiana s
17	1239.5	70.2	Q38777 allium sati
18	1237	70.1	Q9sdy6 glycine max
19	1236	70.0	Q42970 oryza sativ

20	1208.5	68.5	312	10	Q9M7F5	Q9M7F5 arabis pari
21	1208.5	68.5	325	10	P93327	P93327 medicago tr
22	1207.5	68.4	327	10	P94084	P94084 medicago sa
23	1206	68.3	315	10	Q9FXL8	Q9FXL8 psophocarpa
24	1205.5	68.3	305	10	Q9M7H2	Q9M7H2 arabis drum
25	1203.5	68.2	302	10	Q38776	Q38776 allium sati
26	1203.5	68.0	316	10	Q42428	Q42428 castanea sa
27	1198.5	67.9	329	10	O81145	O81145 solanum tub
28	1194.5	67.7	326	10	Q9M7H0	Q9M7H0 arabis fecu
29	1190.5	67.5	335	10	Q9S7J5	Q9S7J5 arabisidopsis
30	1190.5	67.5	335	10	Q9S838	Q9S838 arabisidopsis
31	1189.5	67.4	308	10	Q9M7H4	Q9M7H4 arabis blep
32	1186.5	67.2	315	10	Q43179	Q43179 solanum tub
33	1186.5	67.2	335	10	Q9SXJ4	Q9SXJ4 arabisidopsis
34	1185.5	67.2	302	10	Q9M7G4	Q9M7G4 arabis lemm
35	1185.5	67.2	310	10	Q9M7G9	Q9M7G9 arabis glab
36	1185.5	67.2	335	10	Q9SXJ2	Q9SXJ2 arabisidopsis
37	1185	67.1	320	10	Q9M7G7	Q9M7G7 arabis glab
38	1184.5	67.1	335	10	Q9SXJ3	Q9SXJ3 arabisidopsis
39	1183.5	67.1	306	10	Q9M7G2	Q9M7G2 arabis lign
40	1181.5	66.9	312	10	Q9M7F4	Q9M7F4 arabis pari
41	1180	66.9	311	10	O80404	O80404 cucurbita m
42	1177	66.7	325	10	Q9ZFK4	Q9ZFK4 vitis vinif
43	1174.5	66.5	297	10	Q9FUE3	Q9FUE3 vigna sesqu
44	1171.5	66.4	328	10	Q9ZPI0	Q9ZPI0 cicer ariet
45	1167.5	66.1	329	10	O81144	O81144 solanum tub

ALIGNMENTS

RESULT 1

Q41539 PRELIMINARY; PRT; 320 AA.

AC Q41539; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ENDOCHITINASE PRECURSOR.

GN CHIA1 OR CHI.

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Triticeae; Triticum.

OX NCBI_TaxID=4565;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. CHINESE SPRING;

RA Liao Y.C., Kreuzaler F., Fischer R., Reisener H.J., Tiburzy R.;

RL Plant Sci. 103:177-187(1994).

DR EMBL; X76041; CAA53626.1; -.

DR HSSP; P23951; 2BAA.

DR Mendel; 1463; Triae; Chial; 1463.

DR InterPro; IPR001002; Glyco_hydro_19.

DR Pfam; PF00187; chitin_binding; 1.

DR Pfam; PF00182; Glyco_hydro_19; 1.

DR PRINTS; PR00451; CHITINBINDING.

DR ProDom; PD000574; Glyco_hydro_19; 1.

DR ProDom; PD000609; Chitin_bind; 1.

DR SMART; SM00270; ChtBp1; 1.

DR	PROSITE; PS00774; CHITINASE_19_2; 1.
DR	PROSITE; PS00026; CHITIN_BINDING; 1.
KW	Chitin-binding; Signal.
FT	SIGNAL 1 20 POTENTIAL.
FT	CHAIN 21 320 ENDOCHITINASE.
SQ	SEQUENCE 320 AA; 33602 MW; F258D9DD8EF65E0E CRC64;

Query Match 96.1%; Score 1696.5; DB 10; Length 320;
Best Local Similarity 95.3%; Pred. No. 1.5e-141;
Matches 305; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

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QY 1 MRGVVVVAMLAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTGCQSQCN 60
Db 1 MRGVVVVAMLAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTGCQSQCN 60
QY 61 GCS-GTTPVPVPTPGGGVSSIISSQSLFDQMLLHRNDAAACLAAGFYNYGAFVAAANSFSG 119
Db 61 GCSGGTGPVPTPGGGVSSIISSQSLFDQMLLHRNDAAACLAAGFYNYGAFVAAANSFSG 120
QY 120 FATTGTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNBERGATSDYCTPSSQW 179
Db 121 FATTGADYKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNBERGATSDYCTPSSQW 180
QY 180 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDLVADATVSFKTALFWFMTPOS 239
Db 181 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDLVADATVSFKTALFWFMTPOS 240
QY 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIIINGLECGRGQDGRVADRIGFYKRYC 299
Db 241 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIIINGLECGRGQDGRVADRIGFYKRYC 300
QY 300 DLGVSYGNDLDCYNORPFA 319
Db 301 DLGVSYGNDLDCYNORPFA 320

RESULT 2
Q9AXR9 PRELIMINARY; PRT; 318 AA.
ID Q9AXR9
AC Q9AXR9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 31.7 KDA CLASS I ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000956; AAF04454.1; -.
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINIS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 318 AA; 33636 MW; BA685E1DB7A58B63 CRC64;

Query Match 94.9%; Score 1675.5; DB 10; Length 318;
Best Local Similarity 94.7%; Pred. No. 1.le-139;
Matches 302; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MRGVVVVAMLAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTGCQSQCN 60
Db 1 MRGVVVVAMLAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTGCQSQCN 60
QY 61 GCSGGTGPVPTPGGGVSSIISSQSLFDQMLLHRNDAAACLAAGFYNYGAFVAAANSFSG 120
Db 61 RC-GTTPVPVPTPGGGVSSIISSQSLFDQMLLHRNDAAACLAAGFYNYGAFVAAANSFSAF 119
QY 121 ATTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNBERGATSDYCTPSSQWP 180
Db 120 ATTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNBERGATSDYCTPSSQWP 179
QY 181 CAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDLVADATVSFKTALFWFMTPOS 240
Db 180 CAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDLVADATVSFKTALFWFMTPOS 239
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QY 241 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIIINGLECGRGQDGRVADRIGFYKRYC 300
Db 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIIINGLECGRGQDARVADRIGFYKRYC 299
QY 301 LLGVSYGNDLDCYNORPFA 319
Db 300 LLGVSYGNDLDCYNORPFA 318

RESULT 3
Q9SQL3 PRELIMINARY; PRT; 320 AA.
ID Q9SQL3
AC Q9SQL3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE.
GN CH12.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000956; AAF04454.1; -.
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINIS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 320 AA; 33711 MW; BEFC3ADBFE939B5 CRC64;

Query Match 90.5%; Score 1597; DB 10; Length 320;
Best Local Similarity 90.3%; Pred. No. 8.8e-133;
Matches 288; Conservative 15; Mismatches 14; Indels 2; Gaps 2;

QY 1 MRGVVVVAMLAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTGCQSQCN 60
Db 1 MRGLVVVTILVAAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTGCQSQCN 60
QY 61 GCSGGTGPVPTPS-GGGVSSIISSQSLFDQMLLHRNDAAACLAAGFYNYGAFVAAANSFSG 119
Db 61 GCSGGTGPV-TPTSGGGVSSIVSQSLFEQMLLHRNDAAACLAAGFYNYGAFVAAANSFAG 119
QY 120 FATTGTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNBERGATSDYCTPSSQW 179
Db 120 FGTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNBERGATSDYCTPSSQW 179
QY 180 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDLVADATVSFKTALFWFMTPOS 239
Db 180 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDLVADATVSFKTALFWFMTAQS 239
QY 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIIINGLECGRGQDGRVADRIGFYKRYC 299
Db 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIIINGLECGRGQDGRVADRIGFYKRYC 299
QY 300 DLGVSYGNDLDCYNORPF 318
Db 300 DLGVSYGNDLDCYSORPF 318
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RESULT 4
Q9SQL4 PRELIMINARY; PRT; 340 AA.
AC Q9SQL4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE.
GN Chil.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poae;
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000964; AAF04453.1; -
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChIBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 340 AA; 36011 MW; 3613D7059A871E94 CRC64;

Query Match 88.2%; Score 1557; DB 10; Length 340;
Best Local Similarity 87.9%; Pred. No. 3.1e-129;
Matches 282; Conservative 17; Mismatches 18; Indels 4; Gaps 3;

QY 1 MRGVVVVAMLAFAVSAHAECGSGAQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCN 60
DB 1 MRGLVVVAILVAFAVSAHAECGSGAQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCN 60

QY 61 GCGSGTVPVPTPS-GGGVSSITISQSLFDQMLLRNDAAACLAGFNYCAFVAANSEFG 119
DB 61 GCGSGTVPV-TTPSGGGGVSSIVSLSFEQMLLRNDPSCQANGYTYKAFVAAANSFAG 119

QY 120 FATGSTDVKKREVAFAAQTSHETTGWPTAPDGPYSGYCFNQRGATSDYCTPSSOW 179
DB 120 FGTGSTDVKKREVAFAAQTSHETTGWPTAPDGPYSGYCFNQRGATSDYCTPSSOW 179

QY 180 PCAPGKKGKRGPIQISHNYPGAGQATGTDLLNPDVLASDATVSEKTALEWFWTQPS 239
DB 180 PCAPGKKGKRGPIQISFNYPGAGQATGTDLLNPDVLASDATVSEKTALEWFWTQPS 239

QY 240 KPFSHDVITGRWSPSGADQAGRVPGYVITNIINGLECGRGQDGR--VADRIGFYKR 297
DB 240 KPFSHDVITGRWSPSGADQAGRVPGYVITNIINGLECGRGQDGR--VADRIGFYKR 297

QY 298 YCDLLGVSYGDNLDYCNQRPFF 318
DB 298 YCDLLGVSYGDNLDYCNESPF 320

RESULT 5
Q9FRV1 PRELIMINARY; PRT; 321 AA.
AC Q9FRV1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
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DE SEED CHITINASE-A.
GN RSCA.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohnuma T., Yamagami T., Ishiguro M.;
RT "Cloning and Sequencing of the Rye Seed Chitinase.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051578; BAB18519.1; -
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChIBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 321 AA; 33641 MW; 76E5902BEC337C8E CRC64;

Query Match 80.5%; Score 1421; DB 10; Length 321;
Best Local Similarity 78.9%; Pred. No. 2.8e-117;
Matches 254; Conservative 29; Mismatches 35; Indels 4; Gaps 4;

QY 1 MRGVVVVAMLAFAVSAHAECGSGAQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCN 60
DB 1 MGAFAFAVLAFAVSAHAECGSGAQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCA 59

QY 61 GC-SGGTVP-PVPTPS-GGGVSSITISQSLFDQMLLRNDAAACLAGFNYCAFVAANSEF 117
DB 60 GCGGGTVPVPTPTPSGGGGVSSIVSRALFDRMLLRNDACQAKGFTTYDAFVAAGAF 119

QY 118 SGFATTGSTDVKKREVAFAAQTSHETTGWPTAPDGPYSGYCFNQRGATSDYCTPSS 177
DB 120 PFGTGTGSTDVKKREVAFAAQTSHETTGWPTAPDGAFAFGANGCYCFKRGATSNCTPSA 179

QY 178 QWPCAPGKKGKRGPIQISHNYPGAGQATGTDLLNPDVLASDATVSEKTALEWFWTP 237
DB 180 QWPCAPGKKGKRGPIQISHNYPGAGRAIGVDLLRNPDLVATDTVSFKTAMFWMTA 239

QY 238 QSPKPSHDVITGRWSPSGADQAGRVPGYVITNIINGLECGRGQDGRVADRIGFYKR 297
DB 240 QAPKPSHAVITGQWSPSGTDRAGRVPGVITNIVNGGIECGHGQDSRVADRIGFYKR 299

QY 298 YCDLLGVSYGDNLDYCNQRPFA 319
DB 300 YCDLLRVGYGNLDYCNQRPFA 321

RESULT 6
Q42993 PRELIMINARY; PRT; 323 AA.
ID Q42993
AC Q42993; Q42996;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-
DE POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CH1A1 OR CHT-1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
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OC Eubryotidae: Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPONICA, CV. NIPPONBARE;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
of rice chitinase genes";
RL Mol. Gen. Genet. 241:1-10(1993).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X56787; CAA40107.1; -
DR EMBL; D16222; BAA03750.1; -
DR HSSP; P23951; 2BAA.
DR Mendel; 727; Oryza.Chial;727.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 32
FT CHAIN 33 340
FT CHAIN 33 340 CHITINASE.
SQ SEQUENCE 340 AA; 35586 MW; 642F13E3928CA7BE CRC64;

Query Match 74.6%; Score 1317.5; DB 10; Length 340;
Best Local Similarity 72.4%; Pred. No. 3.8e-108;
Matches 228; Conservative 36; Mismatches 50; Indels 1; Gaps 1;

QY 4 VYVAMIAAFVSAHAECQSGAGGATCPCNLCCKSGFCGTTSDYCTGCGCQSCNGCS 63
Db 16 LVAVLAAALATAAAECQGAAGGARGPCNLCCKSGFCGTTSDYCTGCGCQSCNGC- 74
QY 64 GGTVPVPTPSGGVSSIIQSILFDMLLHRNDAAACLAGFYNYGAFVAAANSFSGFAT 123
Db 75 GGTPTPTPSDGSIVPRLFERLLHRNDGACPARGFYTYEAFLLAAAFAPFAGGT 134
QY 124 GSTDVKREVAFLAQTSHETGGWPTADPGYSWGCYCNQERGATSDYCTPSSOWPCAP 183
Db 135 GNTETKREVAFLGTSHTTGGWPTADPGYSWGCYCNQERGATSDYCTPSSOWPCAP 194
QY 184 GKXFGGPTQISHNYNYGAGQAIGTDLNNPDIVASDATVSKTALFWMTFQSPKPS 243
Db 195 GRKYGGPTQISFNENYAGRAIGYDILLNPDIVATDATVSKTALFWMTFQSPKPS 254
QY 244 SHDVIITGRWSPSGADQAGRVPGYGVITNIINGLEGCGQDGRVADRIGFYKRYCDLLG 303
Db 255 SHDVIITGRWSPSGADQAGRVPGYGVITNIINGLEGCGQDGRVADRIGFYKRYCGAFG 314
QY 304 VSYGDNLDYCNQRPFF 318
Db 315 IGTTGNLDYCNQRPFF 329

RESULT 9
ID P93680 PRELIMINARY; PRT; 326 AA.
AC P93680;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CHIA1 OR CHIA3.
OS Persa americana (Avocado).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
OX NCBI_TaxID=3435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HASS; TISSUE=MESOCARP;
RA Sowka S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,
RX Peterbauer C., Scheiner O., Breiteneder H.,
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z78202; CAB01591.1; -
DR HSSP; P02877; 1HEV.
DR Mendel; 14766; Persea.Chial;14766.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 25
FT CHAIN 26 326
FT CHAIN 26 326 ENDOCHITINASE.
SQ SEQUENCE 326 AA; 34586 MW; 643B20589E062E61 CRC64;

Query Match 73.9%; Score 1305; DB 10; Length 326;
Best Local Similarity 73.2%; Pred. No. 4.6e-107;
Matches 230; Conservative 35; Mismatches 41; Indels 8; Gaps 2;

QY 5 VYVAMIAAFVSAHAECQSGAGGATCPCNLCCKSGFCGTTSDYCTGCGCQSCNGCS 64
Db 10 LLLLLVGLLAGEAFAECQGAAGGALCPGLCCSGFCGTTSDYCTGCGCQSCNGV-- 67
QY 65 GTPVPVPTPSGGVSSIIQSILFDMLLHRNDAAACLAGFYNYGAFVAAANSFSGFAT 124
Db 68 -TPSP-----GGVSLISQSVFNQMLKRNDAACQAKGFYTYNAFNAANSFNGFASVG 121
QY 125 STDVKREVAFLAQTSHETGGWPTADPGYSWGCYCNQERGATSDYCTPSSOWPCAP 184
Db 122 DTATRKREIAAFLAQTSHETGGWPTADPGYSWGCYCNQERGATSDYCTPSSOWPCAP 181
QY 185 KYTFGRGPTQISHNYNYGAGQAIGTDLNNPDIVASDATVSKTALFWMTFQSPKPS 244
Db 182 KKYTGRTQISYNYNYGAGRAIGYDILLNPDIVATDPVISEKTLFWMTFQSPKPS 241
QY 245 HDVITGRWSPSGADQAGRVPGYGVITNIINGLEGCGQDGRVADRIGFYKRYCDLLG 304
Db 242 HNVITGRWTPSAADRAAGRLPGYGVITNIINGLEGCGKGFNDKVDADRIGFYKRYCDLLG 301
QY 305 SYGDNLDYCNQRPFF 318
Db 302 SYGDNLDYCNQRPFF 315

RESULT 10
ID Q42839 PRELIMINARY; PRT; 332 AA.
AC Q42839;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-
ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHIA1 OR CHIA3.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
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RX MEDLINE=96189256; PubMed=8605293;
RA Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
RT "Regulation, expression and function of a new basic chitinase gene in
RL rice (Oryza sativa L.);".
CC Plant Mol. Biol. 30:387-401(1996).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X87109; CAA60590.1; -.
DR HSSP; P23951; 2BAA.
DR Medel; 1634; Oryza; Chial; 1634.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
PT SIGNAL 1 20
SQ SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;

Query Match 72.2%; Score 1274; DB 10; Length 322;
Best Local Similarity 70.8%; Pred. No. 2.4e-104;
Matches 233; Conservative 28; Mismatches 48; Indels 20; Gaps 4;

QY 1 MRGVVVVWVLAFAVSAHAECGSGAGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC- 59
DB 1 MRALAVVVVATFAFAVPEQCGSGAGALCPNCLCCSQYGCWGSTAYCGSGCQSQCS 60
QY 60 -----NGCGSGGVPVPTPSGGVSSIIQSFLDQMLLRNDAACLAKEFYNGAFV 111
DB 61 ROLRRRRDRPSGG-----GGSGVASIVSRSLFDQMLLRNDAACPAKNIYYDAFV 112
QY 112 AAANSFSGFATGSTDVKKREVAFLAQTSHTTGWPTAPDGPYSWGCFNORGAT-- 169
DB 113 AAANAFTFATTGDAATRKREVAFLAQTSHTTGWATAPDGPYSWGCFKEENNGV 172
QY 170 SDYCTPSSOWPCAPKKYGRGPIQISHNYNYPGAGATGTDLLNPDIVASDATVSFKT 229
DB 173 SDYCVQSSQWPCRAKKYGRGPIQISYNYNYPGAGATGNSLLNPDIL-ASDATVSFKT 231
QY 230 ALFWFMTQSPKSSHDVTGRWSPSGAQAGRVPGYGVITNIINGGLECGRGQDGRVA 289
DB 232 AFWFMTQSPKPSCHAVTGWTPNGNDQAGRVPGYGVITNIINGVECGHGADSRVA 291
QY 290 DRIGFYKRYCDLGVSYGNDLCYNORPF 318
DB 292 DRIGFYKRYCDMLGVSYGANLDCYNORPF 320

RESULT 13
Q40667 PRELIMINARY; PRT; 319 AA.
AC Q40667;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE CLASS 1.
GN CHIAI.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y., Baek J., Park H., Choi Y., Kim S.;
RL Biosci. Biotechnol. Biochem. 0:0-0(1994).
DR EMBL; Z29961; CAA62849.1; -.

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DR HSSP; P23951; 2BAA.
DR Medel; 1578; Oryza; Chial; 1578.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 319 AA; 33600 MW; C990572C114FC0A9 CRC64;

Query Match 72.1%; Score 1272.5; DB 10; Length 319;
Best Local Similarity 73.0%; Pred. No. 3.3e-104;
Matches 235; Conservative 29; Mismatches 49; Indels 9; Gaps 5;

QY 1 MRGVVVVWVLAFAVSAHAECGSGAGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
DB 1 MRALAVVVVATFAFAVPEQCGSGAGALCPNCLCCSQYGCWGSTAYCGSGCQSQCS 60
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DB 61 GCGGGGADPA---SGGASGVASIVSRSLFDQMLLRNDAACPAKNFYTYDAFVAANAYP 117
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DB 118 DATTGDAATRKREVAFLAQTSHTTGWATAPDGPYSWGCFKEENNGVSDYCVQS 177
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DB 296 RYCDMLGVSYGANLDCYNORPF 317

RESULT 14
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AC Q41180;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BASIC CHITINASE.
GN CHIAI.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92404740; PubMed=2152343;
RA Neale A.D., Wahlethner J.A., Lund M., Bennett H.T., Kelly A.,
RA Meeks-Wagner D.R., Peacock W.J., Dennis E.S.;
RT "Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in
RT tobacco explants during flower formation.";
RL Plant Cell 2:673-684(1990).
DR EMBL; S44869; AAB23374.1; -.
DR HSSP; P23951; 2BAA.
DR Medel; 14770; Nicot; Chial; 14770.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:21:51 ; Search time 3990.51 Seconds
(without alignments)
3187.393 Million cell updates/sec

Title: US-09-534-229c-6

Perfect score: 771

Sequence: 1 atggcgaggttgctgcct.....agaggaaacttcgtagctag 771

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_om.*

20: em_or.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_ro.*

26: em_sts.*

27: em_sy.*

28: em_un.*

29: em_vi.*

30: em_htgo_hum.*

31: em_htgo_inv.*

32: em_htgo_rod.*

33: em_htg_hum.*

34: em_htg_inv.*

35: em_htg_rod.*

36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	711.8	92.3	1028	8	HVCHT2A	X78671 H.vulgare m
2	659	85.5	1013	8	HVCHT2B	X78672 H.vulgare m
3	654.2	84.9	998	8	AF280438	AF280438 Secale ce
4	636.8	82.6	890	8	HVU276226	AJ276226 Hordeum v
5	559.6	72.6	923	8	ABU16497	ABU16497 Oryza sat
6	474.4	61.3	913	8	OSAF001500	AF001500 Oryza sat
7	395.2	51.3	652	8	RICRCH0	L40338 Oryza sativ
8	329.6	42.7	1186	8	OSLMRNAC	X56787 O.sativa L.
9	307.2	39.7	1291	8	RICCHITA	L37289 Oryza sativ
10	302.8	39.3	1173	8	AF000965	AF000965 Poa prate
11	302.2	39.2	1080	8	AF000966	AF000966 Poa prate
12	301.4	39.1	1985	8	TACHIG	184465 Sequence 2
13	300.6	39.0	1151	6	I84465	D16223 Rice Cht-3
14	296.2	38.4	2808	8	RICCHT3	D16223 Rice Cht-3
15	296.2	38.4	141534	2	AP003685	AP003685 Oryza sat
16	296	38.4	1779	8	BLYCHI33A	L34211 Hordeum vul
17	295.6	38.3	998	8	BLYCHI	M62904 H.vulgare L
18	295.6	38.3	1002	6	A37990	A37990 Sequence 9
19	295.6	38.3	1002	6	AR037574	AR037574 Sequence 9
20	295.6	38.3	1002	6	I75200	I75200 Sequence 9
21	295.6	38.3	3169	8	BLYCHI26A	L34210 Hordeum vul
22	294.6	38.2	1192	8	AF280437	AF280437 Secale ce
23	291.8	37.8	1018	8	AB051579	AB051579 Secale ce
24	283.6	36.8	1252	8	AF000964	AF000964 Poa prate
25	279.6	36.3	138825	8	AC051633	AC051633 Oryza sat
26	278.4	36.1	1160	8	OSENDO	X56063 O.sativa mR
27	278.4	36.1	2739	8	RICCHT1	D16221 Rice Cht-1
28	277.8	36.0	1191	8	AB051578	AB051578 Secale ce
29	277.8	36.0	1684	8	HVU02287	U02287 Hordeum vul
30	273.2	35.4	1051	8	OSU02286	U02286 Oryza sativ
31	269	34.9	1237	8	OSCHIT	X54367 Oryza sativ
32	266.2	34.5	1159	8	OSCHITIA	Z29961 O.sativa LP
33	262.2	34.0	1300	8	AB012855	AB012855 Oryza sat
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36	260.4	33.8	2048	8	OSDNARC24	X87109 O.sativa RC
37	239.6	31.1	1005	8	TOBPRQ	M29868 Tobacco pat
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39	239.6	31.1	1020	6	AR020808	AR020808 Sequence
40	239.6	31.1	1020	6	AR027131	AR027131 Sequence
41	239.6	31.1	1020	6	AR038418	AR038418 Sequence
42	239.6	31.1	1020	6	AR064560	AR064560 Sequence
43	239.6	31.1	1020	6	AR067485	AR067485 Sequence
44	239.6	31.1	1020	6	I07381	I07381 Sequence 31
45	239.6	31.1	1020	6	I38437	I38437 Sequence 7

ALIGNMENTS

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LOCUS	HVCHT2A	1028 bp	mRNA	PLN	01-NOV-1994	
DEFINITION	H.vulgare mRNA for chitinase 2a.					
ACCESSION	X78671					
VERSION	X78671.1	GI:563486				
KEYWORDS	chitinase.					
SOURCE	barley.					
ORGANISM	Hordeum vulgare					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;					
	Poideae; Triticeae; Hordeum.					
	1 (bases 1 to 1028)					
	Bryngelsson,T., Collinge,D.B., Green,B., Gumnesson,P.O., Kragh,K.					
	and Thordal-Christensen,H.					
TTITLE	Purification, characterization and cDNA sequence of a basic					
JOURNAL	chitinase from barley infected with powdery mildew					
REFERENCE	Unpublished					
AUTHORS	2 (bases 1 to 1028)					
	Bryngelsson,T.L.					

```

TITLE      Direct Submission
JOURNAL    Submitted (16-MAR-1994) T.L. Bryngelsson, Department of Plant
           Breeding Research, The Swedish University of Agricultural Sciences,
           S-268 31 Svaloev, SWEDEN
FEATURES   Location/Qualifiers
source     1..1028
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           /dev_stage="seedling"
           /tissue_type="leaf"
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CDS        59..829
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QY 241 cgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
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DEFINITION X78672
ACCESSION  X78672
VERSION    X78672.1 GI:563488
KEYWORDS   chitinase.
SOURCE     barley.
ORGANISM   Hordeum vulgare
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
            1 (bases 1 to 1013)
            Bryngelsson,T., Collinge,D.B., Green,B., Gummesson,P.O., Kragh,K.
            and Thordal-Christensen,H.
            Purification, characterization and cDNA sequence of a basic
            chitinase from barely infected with powdery mildew
            Unpublished
            2 (bases 1 to 1013)
            Bryngelsson,T.L.
            Direct Submission
            Submitted (16-MAR-1994) T.L. Bryngelsson, Department of Plant
            Breeding Research, The Swedish University of Agricultural Sciences,
            S-268 31 Svaloev, SWEDEN
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	QY	598	gtaccggatcacgagtgatcaccaatatcatcaacgcgggcgctcgagtgcggaatgggc	657
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	Db	679	CAGAAGACGCCAACGTCGACCGCATCGGTACTACAAAGCGCTACTCGACATGCTCGGC	738
	QY	718	acggccacccaggaggaacctcgactgctataccaccagaggaaactcgctagctag	771
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LOCUS		Oryza sativa clone MIRCH1	chitinase mRNA,	partial cds.
DEFINITION		AF001500		
ACCESSION		AF001500.1	GI:2109454	
VERSION				
KEYWORDS				
SOURCE		Oryza sativa.		
ORGANISM		Oryza sativa		
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		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
		Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE		1 (bases 1 to 913)		
AUTHORS		Yun,C.-H., Lee,M.-C., Lee,J.S., Yun,K.J. and Eun,M.Y.		
TITLE		Isolation and characterization of a rice chitinase cDNA clone from		
JOURNAL		rice blast fungus-infected rice leaves		
REFERENCE		Unpublished		
AUTHORS		2 (bases 1 to 913)		
TITLE		Yun,C.-H., Lee,M.-C., Lee,J.S., Yun,K.J. and Eun,M.Y.		
JOURNAL		Direct Submission		
		Submitted (29-APR-1997) Dept.of Cyto genetics, National Institute of		
		Agricultural Science and Technology, RDA, Seodundong, Suweon		
		441-707, Korea		
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TITLE	Sequence variation, differential expression and chromosomal location of rice chitinase genes					
JOURNAL	Mol. Gen. Genet.	241	(1-2),	1-10	(1993)	
MEDLINE	94049667					
REFERENCE	2	(bases 1 to 1186)				
AUTHORS	Nishizawa,Y					
TITLE	Direct Submission					
JOURNAL	Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF AGRONOMICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI 305, JAPAN					
FEATURES	Location/Qualifiers					
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Dd	459	GACCTCCACAGAACACCGCGGGTGGCCACACCGCGCGCGCGCTTCTCTCTCGGG	518			
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Dd	519	CTACTGTCTCAAGCAGAGAGAACCOCGCTCGACTACTGCCAGCOCTCGCGGAGTG	578			

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Qy	465	gtcacggaacggtggtgtccttcaggaacggccatgtggtttcgttgatgacggcgaggg	524
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Db	759	GAACAACCGTCGAGCACGACGTATACCGGCGGTGGCGCTCGCGCGCGGACGC	818
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Qy	645	qtgcggaatggccgaacagcgcacacgttcgacgcgcatcgctactactacacgcgctactg	704
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Qy	705	cggcatgctcgcgcagcgccacgcgaggcaacctgcagtctacacccagagaacctcgc	764
Db	939	TGGCGGTTCGCATCGSCACCGCGGCAACCTCGACTGCTACACACGAGGCGCTTCAA	998
Qy	765	tagc 768	
Db	999	CAGC 1002	
RESULT 9			
R1CCHITA			
LOCUS	R1CCHITA	1291 bp	mRNA PLN 30-OCT-1994
DEFINITION	Oryza sativa chitinase mRNA, complete cds.		
ACCESSION	L37289		
VERSION	L37289.1	GI:561872	
KEYWORDS	chitinase.		
SOURCE	Oryza sativa (strain IR36)	seedling etiolated leaf cdna to mRNA.	
ORGANISM	Oryza sativa		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza. Yun,C.-H., Kim,J.-K. and Park,Y.-H. 1 (bases 1 to 1291) Isolation and Characterization of A Rice Chitinase cDNA Unpublished (1994)			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES	Location/Qualifiers		
source	1..1291		
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sig_peptide	43..111		
CDS	43..1044		
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Db 907 TCCCAAGCCTTCGAGCCAGCGCGTGATCACCGGCGAGTGAGGCCCTCGGCGCGAGACCA 966
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Db 1027 GTGCGGCAAGGGGAGGACACACCGCGTCCGCGGAGGATCGGTTCTACAGCGCTACTG 1086
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Db 1087 CGACTCTCGGCGTACGCTACGGGGACACCTGGACTGCTACACGAGAGCGGTTCAA 1146
QY 765 tagcta 770
Db 1147 TGGTTA 1152

RESULT 11
AF000966
LOCUS AF000966 1080 bp DNA PLN 31-OCT-1999
DEFINITION Poa pratensis chitinase (Chi2) gene, complete cds.
ACCESSION AF000966
VERSION AF000966.1 GI:6164587
KEYWORDS .
SOURCE Kentucky bluegrass.
ORGANISM Poa pratensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poae; Poa.
AUTHORS Du, M. and Ha, S.B.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley, CA
94706, USA

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28..990
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BASE COUNT 208 a 366 c 327 g 179 t
ORIGIN

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Best Local Similarity 65.3%; Pred. No. 2.7e-32;
Matches 498; Conservative 0; Mismatches 223; Indels 42; Gaps 2;

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Db 227 CGGTGACCCGACTCCCTCGCGGCGCGGCGGTCTCTCATGTAATCATGTCGTCTCT 286
QY 110 acgcagcactatgcccaacgcagcaactcgtgtgtccgcgcgcgcgcgcgcgcgcgcgcgc 169
Db 287 TCGAGCAGATGCTTCTGCACCGCAACGACGCGCATGCTCTGGCCAGGGTTTCTACACCT 346
QY 170 acgacaccttcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 229

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Db 347 ACAAGCCTTCATCGCCGCCGCCCAACTCTTTGGCGGTTTGGGACCAACGAGCAGCACCG 406
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QY 347 gc-----aaggccacgtcccccacat 367
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QY 368 actatgacgggggaccatcccaattgacaggcggtccaaactacgactctgcccgggagag 427
Db 587 ACTTCGCGCGGGGCCCATCCAGATCTCTTACAACACTACACTAGGCGCAGCGGAGG 646
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Db 647 CCATCAAACTGACCTGCTCAACAACCCGACCTTGTGGCCACAGACCCGACCGTGTCT 706
QY 488 tcaggacggccatgtgttctggtatgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 547
Db 707 TCAAGACGGCGCTGTGTTCTGATGACGCTCAGTCGCGCAAGCGCTGAGCGCGCG 766
QY 548 tgcctatcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 607
Db 767 TGATCACCGCGCAGTGGAGCCCTCGAGCGCAGACCAAGCGGCGGAGGTGCGCGGT 826
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QY 728 gaggaacgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 770
Db 947 GAACACCTGGACTGTACAGCCAGAGCGCGTTCGGGTAGTTA 989

RESULT 12
TACHIG 1985 bp DNA PLN 02-AUG-1996
LOCUS T.aestivum (Chinese spring) chi gene for endochitinase.
DEFINITION T.aestivum (Chinese spring) chi gene for endochitinase.
ACCESSION X76041
VERSION X76041.1 GI:416028
KEYWORDS CHI gene; endochitinase.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1985)
AUTHORS Liao, Y.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH,
Worringer Weg, 52056 Aachen, FRG
REFERENCE 2 (bases 1 to 1985)
AUTHORS Liao, Y.C., Kreuzaler, F., Fischer, R., Reisenner, H.J. and Tibury, R.
TITLE Characterization of a wheat class Ib chitinase gene differentially
induced in isogenic lines with infection with Puccinia graminis
JOURNAL Plant Sci. 103, 177-187 (1994)
FEATURES
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71..1595
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DEFINITION	Oryza sativa chromosome 6 clone P0548E04, *** SEQUENCING IN PROGRESS ***, in ordered pieces.				
ACCESSION	AP003685				
VERSION	AP003685.1	GI:14192855			
SOURCE	HTG; HTGS_PHASE2;				
ORGANISM	Oryza sativa (cultivar:Nipponbare) DNA, clone:P0548E04. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza.				
REFERENCE	1 (sites)				
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.				
TITLE	Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0548E04				
JOURNAL	Published Only in DataBase (2001) In press				
REFERENCE	2 (bases 1 to 141534)				
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakia@abrr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel.:81-298-38-7441, Fax:81-298-38-7468) NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.				
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	/cultivar="Nipponbare"				
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	/clone="P0548E04"				
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ORIGIN					
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Best Local Similarity	66.1%;	Pred.No. 1.8e-32;			
Matches	483; Conservative	0; Mismatches 203;	Indels 45; Gaps	2;	
QY	79 gggtgggcttgatcaccgcagcggttctacacgaacttcgccacccaggcaaac	138			
Db	19831 GGCGTCGCCCTCCATCATATGCCTCCTTGTGGACCAGATGCTGCTCCACCGCACGAC	19772			
QY	139 tcgctgtgcccgcccagaggtttcacacgaacttcacgcacctcatcgccgcgcacaac	198			
Db	19771 CAGGCGTGCCCGCCTTAGGGCTTTCTACACTACGAGCGCTTCGTGCGCGCGCCACAGCC	19712			
QY	199 ttccccgggttcggcaccaccgcagcgccgacgacatacaagaagcgaactgcgcgcattc	258			
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QY	259 ttgcggccagactcccaacagacaaacccggag---	315			
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QY	364 -----ccatactatgaacggggagccaccatcaaatty	393			
Db	19531 AAGCGGGAGTGGCCGTGGCGCGCGCAAGAGTACTACGGCCCGGGGACCCATCAGATC	19472			

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:36:06 ; Search time 309.71 Seconds
(without alignments)
2134.247 Million cell updates/sec

Title: US-09-534-229c-6

Perfect score: 771

Sequence: 1 atggcgaggtttgcgcct.....agaggaacttgcgtagtag 771

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 segs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	651.2	84.5	756	20	AA24890 Rye chitinase-like
2	470.6	61.0	1013	21	AA96231 cDNA encoding a ma
3	327.4	42.5	1077	21	AA96230 cDNA encoding a ma
4	300.6	39.0	1151	13	AAQ31408 RCH10 chitinase ge
5	300.6	39.0	1151	16	AAQ81346 Rice chitinase RCH
6	299.4	38.8	954	20	AA24889 Rye chitinase-like
7	297.4	38.6	3035	22	AAF54983 Nucleotide sequenc
8	295.5	38.3	1002	15	AAQ62518 Sequence encoding
9	262.2	34.0	1318	19	AAV49982 Floral organ-speci
10	246	31.9	1163	21	AA96224 cDNA encoding a ma
11	239.6	31.1	1010	11	AAQ06185 PR-Q cDNA cloned i

12	239.6	31.1	1020	10	AA90845 Tobacco PR-Q gene.
13	239.6	31.1	1020	20	AAV62809 Tobacco PR-Q gene
14	239.6	31.1	1020	20	AAV72995 PR-Q protein encod
15	235.4	30.5	965	12	AAQ12897 Petunia extracellu
16	235.4	30.5	966	18	AA789951 Petunia hybrida ex
17	235.4	30.5	966	21	AA58909 cDNA sequence enco
18	218.2	28.3	968	11	AAQ06186 PR-P cDNA cloned i
19	218.2	28.3	968	20	AAV62813 Tobacco PR-P gene
20	218.2	28.3	968	20	AAV62813 PR-P protein encod
21	213.2	27.7	4704	11	AAQ05264 cDNA encoding a ma
22	200.2	26.0	1118	18	AA96233 Chitinase coding s
23	199.6	25.9	879	18	AA77940 Full length chitin
24	199.6	25.9	996	18	AA77941 cDNA encoding a ma
25	198.6	25.8	583	21	AA96234 Banana ripening fr
26	196.4	25.5	7397	20	AA25613 Wild tomato endoch
27	193.4	25.1	966	16	AAQ93034 Wild tomato endoch
28	190.2	24.7	935	16	AAQ93035 American elm chiti
29	185	24.0	1225	17	AA73325 Tobacco intracellu
30	159	20.6	1152	12	AAQ12898 Nicotiana sp. intr
31	159	20.6	1152	18	AA789952 cDNA sequence enco
32	159	20.6	1152	21	AA58910 Banana fruit ripen
33	158.8	20.6	721	20	AAV69461 Floral organ-speci
34	153.8	19.9	2636	19	AAV49983 Sequence encoding
35	153.6	17.6	1153	13	AAQ21007 Endochitinase prec
36	135.6	17.6	1153	15	AAQ68352 Sequence of chimer
37	135.6	17.6	1160	13	AAQ21193 Sequence of chimer
38	135.6	17.6	1863	13	AAQ74261 Tomato-tobacco end
39	135.6	17.6	1863	15	AAQ74261 Potato infection i
40	129.6	16.8	501	21	AAA40411 Chitinase gene con
41	129.2	16.8	3850	12	AAQ11093 Basic chitinase ge
42	129.2	16.8	3850	12	AAQ15147 Banana fruit ripen
43	129	16.7	755	20	AAV69463 Rye chitinase-like
44	121.4	15.7	292	20	AA24892 cDNA encoding a ma
45	119.8	15.5	1048	21	AA96232

ALIGNMENTS

RESULT 1

AA24890
ID AAX24890 standard; cDNA; 756 BP.

XX AAX24890;

AC AAX24890;

DT 21-JUN-1999 (first entry)

XX Rye chitinase-like protein CHT46 cDNA clone ch-46.

XX CHT46; chitinase-like protein; antifreeze protein; AFP;

KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;

KW transgenic plant; preservation; cryopreservation; tumour; therapy;

KW ss.

OS Secale cereale.

XX Key Location/Qualifiers

FT CDS 1..756

FT /*tag= a

FT /note= "separately claimed in Claim 2"

FT sig_peptide 1..66

FT /*tag= a

FT mat_peptide 67..756

FT /note= "separately claimed in Claim 2"

FT WO9906565-A2.

PD 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

[illegible]

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Db	922	gccagccgagtcggtcttcaagcgtactcgacatcctcgctcgctcagctacggcgcc 981
QY	733	aactcgaactgtcaccccgaggaactcgct 765
Db	982	aacttgatgtctacgccagggccttcggt 1014
RESULT	6	
ID	AAx24889	standard; cDNA; 954 BP.
AC	AAx24889;	
XX		
DT	21-JUN-1999	(first entry)
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DE	Rye chitinase-like protein CHT9 cDNA clone ch-9.	
XX		
KW	CHT9; chitinase-like protein; antifreeze protein; AFP;	
KW	winter rye; antifungal; fungicide; cold tolerance; frost tolerance;	
KW	transgenic plant; preservation; cryopreservation; tumour; therapy;	
SS		
OS	Secale cereale.	
XX		
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FT		/note= "separately claimed in Claim 2"
FT	sig_peptide	1..60
FT		/*tag= a
FT	mat_peptide	61..954
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XX		
PN	WO990565-A2.	
XX		
PD	11-FEB-1999.	
XX		
PF	31-JUL-1998;	98WO-CA00745.
XX		
PR	31-JUL-1997;	97US-0903872.
XX		
PA	(ICEB-) ICE BIOTECH INC.	
XX		
PI	Griffith M, Hew C, Moffatt B, Xiong F;	
DR	WPI; 1999-153795/13.	

KW beta-1,3-glucanase activity; pest resistance; ss.

XX Nicotiana sp.

XX US5847258-A.

XX 08-DEC-1998.

XX 31-MAY-1995; 95US-0457364.

XX 31-MAY-1995; 95US-0457364.

XX 08-MAR-1988; 89US-0156687.

XX 06-FEB-1989; 89US-0305566.

XX 24-MAR-1989; 89US-0329018.

XX 20-MAR-1989; 89US-0368672.

XX 20-OCT-1989; 89US-0425504.

XX 07-SEP-1990; 90US-0580431.

XX 21-DEC-1990; 90US-0632441.

XX 01-APR-1991; 91US-0678378.

XX 27-SEP-1991; 91US-0768122.

XX 06-MAR-1992; 92US-0848506.

XX 06-NOV-1992; 92US-0973197.

XX 06-APR-1993; 93US-0042847.

XX 12-APR-1993; 93US-0045957.

XX 16-JUL-1993; 93US-0093301.

XX 13-JAN-1994; 94US-0181271.

XX (NOVS) NOVARTIS FINANCE CORP.

XX Moyer MB, Bayne GB, Ryals JA, Ward ER;

XX WPI; 1999-059180/05.

XX DNA encoding pathogenesis-related glucanase proteins - useful for producing transgenic plants with enhanced disease or pest resistance

XX Example 46; Column 171-174; 169pp; English.

XX The present invention describes a DNA molecule encoding a

XX pathogenesis-related (PR) protein having beta-1,3-glucanase activity

XX selected from PR-2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described

XX are: (i) a chimeric gene comprising the above DNA molecule linked to a

XX heterologous promoter; (ii) a vector containing the chimeric gene;

XX (iii) a host cell containing the chimeric gene; (iv) a transgenic plant

XX containing the chimeric gene; and (v) a seed from the transgenic plant.

XX The DNA molecule is used to produce transgenic plants with enhanced

XX disease or pest resistance. The present sequence represents a tobacco

XX PR-Q protein encoding cDNA sequence from the present invention.

XX Sequence 1020 BP; 310 A; 181 C; 240 G; 289 T; 0 other;

Query Match 31.1%; Score 239.6; DB 20; Length 1020;
Best Local Similarity 61.3%; Pred. NO. 7.8e-34;
Matches 424; Conservative 0; Mismatches 259; Indels 9; Gaps 2;

QY 72 ggcgcaggcggtggcggtcgcacgcggtcggtgtacgcgagcactctgcccaacg 131

Db 105 ggcacagcattgtgtctattgttaacagtgactgttcaacgagatgctgaagaatag 164

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QY 192 caacaccttcocggcttgcgcacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 251

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QY 372 tggacggggaccatcccaattgacagggcggtccaaactacgatcttgcgggagagcgat 431

Db 396 tggtagaggaccatcccaattgacaaacggaataaactatgagaagctggaactgcaat 455

QY 432 cgggaaggacctggtgagcaaccagacctagtgtccacgacgcggtggtgtccttcag 491

Db 456 tggacaagagtagttaacacaccccttgattgtggccacagatgctactatatactcaa 515

QY 492 gacggccatgtggttctggtgacggcgacgggaaacaaagcgtgtgtcccaacgctgc 551

Db 516 aacagctatgtgttggtagacaccacaggaacaaacgcatcttccacgacgttat 575

QY 552 cctacgcgtgtgacgc 611

Db 576 catcgtcgttggactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 635

QY 612 agtgatcacaatatcatcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 671

Db 636 tgtaattacacacatcattaaacgggaattgaaatgtgcatagacaggaatgacgcagt 695

QY 672 cgtcgc 731

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QY 732 caacctgcactgctacacccagaggaacttcg 763

Db 756 aaacttgactgttac 787

RESULT 15

AAQ12897

ID AAQ12897 standard; cDNA; 965 BP.

XX AC AAQ12897;

XX DT 14-OCT-1991 (first entry)

XX DE Petunia extracellular chitinase gene.

XX KW fungal resistance; phytopathogen; ss.

XX OS Petunia hybrida.

XX Key Location/Qualifiers

FT sig_peptide 25..93

FT mat_peptide 94..786

FT /tag= a

FT /tag= b

FT /product= extracellular chitinase

XX EP440304-A.

XX PD 07-AUG-1991.

XX PF 30-JAN-1991; 91EP-0200191.

XX PR 30-JAN-1990; 90NL-0000222.

XX PA (MOGE-) MOGEN INT NV.

XX PA (OYLE-) RIJKSUNIV TE LEIDEN.

XX PI Cornelissen BJ, Melchers LS, Meulenhoff EJ, Van Roekel JS;

XX PI Sela-Buurlage MB, Vloemans AA, Woloshuk CP, Bol JF;

XX WPI; 1991-232019/32.

XX DR P-PSDB; ARI13274.

XX PT Plants with improved resistance to pathogenic fungi - contains

XX chitinase and/or beta-1,3-glucanase genes modified for

XX over-expression targeted to apoplasts

```
XX Example 4; Fig 1; 55pp; English.
PS
XX This sequence was isolated from a p.hybrida cDNA library. It has 80
CC per cent homology with tobacco clone PROB30 which encodes
CC extracellular chitinase PR-Protein R. The gene can be inserted into
CC an appropriate plasmid for production of transgenic plants having
CC resistance to fungal pathogens.
CC See also AA012898-Q12900.
XX
SQ Sequence 965 BP; 300 A; 173 C; 218 G; 274 I; 0 other;

Query Match      30.5%; Score 235.4; DB 12; Length 965;
Best Local Similarity 59.7%; Pred. No. 4.2e-33;
Matches 414; Conservative 0; Mismatches 276; Indels 3; Gaps 1;

QY 72 ggcgcaggcggcgtgcgtacacgcgggtgtaacgcgagcaactctgccaaacg 131
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QY 132 cgacaactcgtctgccgcgcagaggggtctacacgtacacgccttcacgcgcgcgc 191
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Db 150 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 210 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 252 cgcctcttcgcgcgcacacctccacagacaccgcgcgcgcgcgcgcgcgcgcgcgcgc 311
Db 252 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 432 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 492 gacggccatgtggttcgtgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 551
Db 492 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 507 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 567 caccgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 626
Db 567 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 612 agtgataccaataatcacaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 671
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Db 627 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 687 ggaagatcgaattggatattacacaggggaattgaattgaattgaattgaattgaattgaatt 746
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QY 732 caacctgcactgtacacccagaggaacttcgc 764
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QY 747 caatttgattgtacaaccaaggaactttgc 779
Db 747 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: May 3, 2002, 16:32:02
Job time: 6956 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:25:26 ; Search time 142.45 Seconds
(without alignments)
1225.795 Million cell updates/sec

Title: US-09-534-229C-6

Perfect score: 771

Sequence: 1 atgcgaggttgctgcct.....agaggaaactcgtagctag 771

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCNUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300.6	39.0	1151	1	US-07-704-288C-2
2	300.6	39.0	1151	1	Sequence 2, Appli
3	300.6	39.0	1151	1	Sequence 1, Appli
4	295.6	38.3	1002	1	Sequence 2, Appli
5	295.6	38.3	1002	1	Sequence 9, Appli
6	295.6	38.3	1002	1	Sequence 9, Appli
7	239.6	31.1	1020	1	Sequence 9, Appli
8	239.6	31.1	1020	1	Sequence 7, Appli
9	239.6	31.1	1020	1	Sequence 7, Appli
10	239.6	31.1	1020	1	Sequence 7, Appli
11	239.6	31.1	1020	1	Sequence 7, Appli
12	239.6	31.1	1020	1	Sequence 7, Appli
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17	239.6	31.1	1020	2	Sequence 7, Appli
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19	239.6	31.1	1020	2	Sequence 7, Appli
20	239.6	31.1	1020	4	Sequence 7, Appli
21	235.4	30.5	966	1	Sequence 8, Appli
22	235.4	30.5	966	3	Sequence 8, Appli
23	235.4	28.3	968	1	Sequence 8, Appli
24	218.2	28.3	968	1	Sequence 12, Appl
25	218.2	28.3	968	1	Sequence 12, Appl
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37 218.2 28.3 968 4 US-09-350-600-12 Sequence 12, Appli
38 195 25.3 966 1 US-08-162-475A-1 Sequence 1, Appli
39 190.2 24.7 935 1 US-08-162-475A-3 Sequence 3, Appli
40 185 24.0 1225 1 US-08-286-020-1 Sequence 1, Appli
41 185 24.0 1225 1 US-08-603-919-1 Sequence 1, Appli
42 160.2 20.8 943 2 US-08-475-427-15 Sequence 15, Appli
43 160.2 20.8 943 2 US-07-842-165-15 Sequence 15, Appli
44 159 20.6 1152 1 US-08-047-413-10 Sequence 10, Appli
45 159 20.6 1152 3 US-08-229-050-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-07-704-288C-2
; Sequence 2, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 39.0%; Score 300.6; DB 1; Length 1151;
Best Local Similarity 65.6%; Pred. No. 1.1e-51;
Matches 494; Conservative 0; Mismatches 214; Indels 45; Gaps 2;

[illegible]

8
PESNT.T

US-08-449-315-7
Sequence 7, Application US/08449315
Patent No. 5650505
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF

TS-08-449-315-7

Query Match	31.18;	Score 239.6;	DB 1;	Length 1020;
Best Local Similarity	61.38;	Pred. No. 1.3e-39;		
Matches 424;	Conservative	0;	Mismatches 259;	Indels 9;

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Qy	132	cgacaactcgtgtgcgcgcgcagaggggttcacagttacgtaacgtaacgaccttcacgcgcgcgc	191
Db	165	GAACGACGGTAGATGCTCGCAATGGCTTCTACATTATGATGCAATTCTATGCTGCTGC	224
Qy	192	caacacctcccggcgttcggccaccacgcgcgcgcgcgcacatcaacgcgcgcactcgc	251
Db	225	CAATTCCTTTCTCGTGTTCGGAACTACTGGTGATGATATGCTCCGTAGAAAGAAATTCG	284
Qy	252	cgctcttcggcgcagacctccacagacacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	311
Db	285	TGCCTTTTTCGGTCAAACTCTCACGAACTACTGGTGGATCCCTGAGTGCAG--AACCA	342
Qy	312	gtccagtggggcctactgcttcagggaagagataagcaaggcccaactccccaccactacta	371
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Qy	372	tggacggggacccatccaatgacagggcggttccaaactacgatctctgcgcgggagagcgat	431
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Qy	432	cgggaagagacctggtgagcaaccacagacctagttgtccacgcgcgcgcggtgtgtctcttcag	491

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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/COC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-444-803-7

Query Match 31.1%; Score 239.6; DB 1; Length 1020;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9; Gaps

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QY 312 gtccagtygggctactgcttccaagggaagagataaagcaaggccacgtcccaaccatacta 371
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QY 612 agtataccaatatcatcaacgcggcggtctcgagtgcgggaatggccgggaacacgaccaa 671
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Db 696 GGAAGATCGAATGGATATACAGGAGGATTTGTTGTTATTTAAATTTCTCGGGGGGA 755
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RESULT 12

US-08-455-416-7

Sequence 7, Application US/08455416

Patent No. 5777200

GENERAL INFORMATION:

APPLICANT: Ryals, John A.

APPLICANT: Alexander, Danny C.

APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.

APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.

APPLICANT: Harms, Christian

APPLICANT: Meins, Jr., Frederick

APPLICANT: Montoya, Alice

APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-Marc

APPLICANT: Payne, George B.

APPLICANT: Sperison, Christoph

APPLICANT: Stinson, Jeffrey R.

APPLICANT: Uknes, Scott J.

APPLICANT: Ward, Eric R.

APPLICANT: Williams, Shericea C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-455-416-7

Query Match 31.1%; Score 239.6; DB 1; Length 1020;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9; Gaps 2;

QY 72 ggcgcaggcgctggcgctcgctacacgcgctcggtgtacgcgagcactctgcccacacg 131
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US-08-455-244-7

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Query Match          31.1%; Score 239.6; DB 1; Length 1020;
Best Local Similarity 61.3%; Pred. NO. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9; Gaps 2;

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DB 105 GGCACAGGCATTGGTTCTATTGTAACAGAGTGACTTGTCAACGAGATGCTGAAGATAG 164
QY 132 cgacaactcgcctgtcccgccagagggttctacacgtacagaccccttcacgcgcgcg 191
DB 165 GAACGACGGTAGATGTCTCTGCCAATGGCTTCTACACTATGATCATTCATAGCTGTGC 224
QY 192 caacaccttccgggcttcggccacacgcgcgcgcgcgcacatcaagcgcgcacctgcg 251
DB 225 CAATTCCTTCTCGTTTGGAACTACTGGTGATGATGACTCCCGTAGGAAGAAATGTC 284
QY 252 cgccttcttcggccagacctctccacgagacacccggaggagcagagcgtgcgcgcgc 311
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QY 312 gttccagtgggctacgtcttcaaggaagagatgaagaagcgcgcgcgcgcacatacta 371
DB 343 TTPACAGAGGGTATGCTTTGTTAGCCAAATGACCAGATGAGC-----AGATATTA 395
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DB 396 TGGTAGAGGACCCATCCAAATTGACAAACCGAAATAACTATGAGAAAGCTGGAACCTGCA 455
QY 432 cgggaagagacctggtgagcaaccacgaacctagtgtccacgagcgcggtgggtctcctc 491
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QY 492 gacggcgcgtggttctcgatgacggcgaggggaaacgaagccgtcggtgccacaacgtgc 551
DB 516 AACAGCTATATGGTTTGGATGACACCACAGGACAAACAGCCATCTTCCACGACGTAT 575
QY 552 cctacgcgcgtggagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 511
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QY 612 agtgatcaccaatatcatcaacgcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 671
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DB 756 AAACITGGACTGTTACACCAAGGAACTTCG 787

RESULT 14
US-08-454-876-7
; Sequence 7, Application US/08454876
; Patent No. 5804693
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.

```


GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:24:00 ; Search time 3076.35 Seconds
(without alignments)
2693.125 Million cell updates/sec

Title: US-09-534-229C-6

Perfect score: 771

Sequence: 1 atggcgaggttgctgcct.....agaggaaactcgctagtag 771

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	661.6	85.8	906	11	BF065825 HV_CEB001
2	623.6	80.9	824	11	BF064990 HV_CEB002
3	597.6	77.5	937	10	BE559387 HV_CEB002
4	589.2	76.4	923	11	BF065694 HV_CEB001
5	569.6	73.9	829	11	BF065067 HV_CEB002
6	568.6	73.7	936	11	BF066058 HV_CEB001
7	562.4	72.9	842	11	BF264498 HV_CEB000
8	545.4	70.7	669	10	BE215473 HV_CEB000
9	538.6	69.9	695	10	BE214577 HV_CEB000
10	523.6	67.9	725	10	BE214283 HV_CEB000
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17	425	55.1	541	11	BF257510	BF257510 HVSMEF001
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22	388.6	50.4	875	11	BF623602	BF623602 HVSMEA000
23	387.2	50.2	466	10	BE586541	BE586541 WHF0505_G
24	362.4	47.0	505	10	BE215793	BE215793 HV_CEB000
25	355.6	46.1	457	10	BE420363	BE420363 WWS05_G8R
26	346	44.9	753	11	BF259671	BF259671 HVSMER001
27	341.2	44.3	793	11	BF624096	BF624096 HVSMER000
28	337	43.7	628	10	BE493038	BE493038 WHF0562_G
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31	286.6	37.2	1123	11	BF262973	BF262973 HV_CEB000
32	278.8	36.2	805	11	BF655536	BF655536 HVSMER1000
33	255.4	33.1	954	11	BF265189	BF265189 HV_CEB001
34	250	32.4	472	11	C72797	C72797 C72797 Rice
35	239.6	31.1	574	10	AW461042	AW461042 707097F10
36	238.4	30.9	729	10	BE602672	BE602672 HVSMER010
37	237.8	30.8	681	10	BF705117	BF705117 Sc02_08b0
38	236.2	30.6	912	11	BF301220	BF301220 HVSMER001
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40	233.6	30.3	742	11	BF365634	BF365634 HVSMER1000
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ALIGNMENTS

RESULT 1	BF065825	906 bp	EST	09-MAR-2001
LOCUS	HV_CEB0014B14f	Hordeum vulgare seedling green leaf EST library		
DEFINITION	HVCNDA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone			
	HV_CEB0014B14f, mRNA sequence.			
ACCESSION	BF065825			
VERSION	BF065825.2	GI:13265390		
KEYWORDS	EST.			
SOURCE	barley.			
ORGANISM	Hordeum vulgare			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae			
	; Triticeae; Hordeum.			
REFERENCE	1 (bases 1 to 906)			
AUTHORS	Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.			
TITLE	Development of a genetically and physically anchored EST resource for barley genomics			
JOURNAL	Unpublished (2000)			
COMMENT	On Oct 17, 2000 this sequence version replaced gi:10842464. Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: AATTACCTCCTCACTAAGG High quality sequence stop: 749. Location/Qualifiers 1..906 /organism="Hordeum vulgare"			

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

REFERENCE
AUTHORS

1 (bases 1 to 923)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.

TITLE

Development of a genetically and physically anchored EST resource
for barley genomics

JOURNAL
COMMENT

Unpublished (2000)
On Oct 17, 2000 this sequence version replaced gi:10842333.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTAACCTCCTAATAAGGG

High quality sequence stop: 640.

FEATURES

Location/Qualifiers

source

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/organism="Hordeum vulgare"
/cultivar="Cil16151 (M1a6)"
/db_xref="taxon:4513"
/clone="HV_CEB0013H08f"
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library HVCDNA0005 (Erysiphe infected & control))
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT
ORIGIN

194 a 277 c 282 g 170 t
Query Match 76.43; Score 589.2; DB 11; Length 923;
Best Local Similarity 87.28; Pred. No. 9.5e-104;
Matches 670; Conservative 0; Mismatches 93; Indels 5; Gaps 2;

Qy 1 atggcgaggttgctgcctcgccgtgtgaccccgccgtccctgctgcgcgtgcgcg 60
Db 42 ATGGCGAGGCTGTGCTCCCTGCGGTGTGCGCCCGCCGCTCCCTGCTGCGCGCGGTG 101
Qy 61 gggggtgc 120
Db 102 GCATG 161
Qy 121 ctgcccacccgcgaactcgtgtgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
Db 162 CTGCCCCAACCCGCGCAACTGCTGTGCCCGCCGCGCGCGCGCGCGCGCGCGCTC 221
Qy 181 atgc 240
Db 222 ATCGCGCGGACGACACACTTTCGGGCTTCGGCACCACCGCGCGCGCGCGCGCATCAAG 281
Qy 241 cgcgacctgc 300
Db 282 CGCGAGCTCGCGCGCTTTCGGCCAGACCTCCACGAGACCCACCGGAGGACGAGAGGC 341
Qy 301 gctaccacagttccagtgggtactgttcaaggagagagagagagagagagagagag 360
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Qy 361 ccaccatactgagcgggggaccatccaatgtacagggcggttcaactacgattctgcc 420
Db 402 CCACCTACTATGACGGGGACCCATCCAAATTGACAGGGCGGTCCAACTAGATCTGCC 461
Qy 421 gggagagcgtcgggaaggaactggtgagcaaccacgacctagtgtccacggcgggtg 480
Db 462 GGGAGAGCGATCGGAGGAGGACCTTGTGAGCAACCGGATCTGTTCTCCACGCGCGGTG 521

Qy 481 gtgtccttcaggacgcccattgtgttctgatatcagcgcgaggaacaaacgctctgc 540
Db 522 GTGTCTTTAAGACGGGATGTGTGTCTGTGATGACGCGCAGGCAACAGCCGTCGAGC 581
Qy 541 cacaacgtccctacacgcgcgtgacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600
Db 582 CACAACGTCGCTACGCGCTGACGCGCGCGACGCGCGCGCGCGCGCGCGCGCGCTGCGGTT 641
Qy 601 ccggtatcagagtgatcaccaatatcatcaacgcgcggtcagtgcggaalggccc-- 658
Db 642 CCAAGCTACGCTGTAATCACATATTTATTCACGGCGCGGCTTCAATCGGATGGGCCCG 701
Qy 659 ggaacgacgcccacgctgc 715
Db 702 GAACCGACCCCAACGCTCGAATGATGTTGTTGTTACTTAAAGCCCTTATGAGGATGCTGG 761
Qy 716 gcaacgcccacgaggaacacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 763
Db 762 GGACGGGACACGAGGCAAACTTGTATGTTGTTAAACCAACCAAGGAACCTTG 809

RESULT 5
BF065067/c
LOCUS
DEFINITION
BF065067 829 bp mRNA EST 09-MAR-2001
HV_CEB0022N01f Hordeum vulgare seedling green leaf EST library
HV_CEB0022N01f (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEB0022N01f, mRNA sequence.
ACCESSION
BF065067
VERSION
BF065067.1 GI:10841706
KEYWORDS
EST.
SOURCE
barley.
ORGANISM
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 829)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE
Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL
Unpublished (2000)
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCCTAATAAGGG
High quality sequence stop: 589.
Location/Qualifiers
1..829
/organism="Hordeum vulgare"
/cultivar="Cil16151 (M1a6)"
/db_xref="taxon:4513"
/clone="HV_CEB0022N01f"
library HVCDNA0005 (Erysiphe seedling green leaf EST
library HVCDNA0005 (Erysiphe infected & control))
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT 145 a 247 c 270 g 167 t
ORIGIN

Query Match 73.9%; Score 569.6; DB 11; Length 829;
Best Local Similarity 90.9%; Pred. No. 5.4e-100;


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Db 751 CGGAAGAGCGCCCAAGCTCAATCCGCTTGGGTACTTAACACACGGCCTACTGCGGGAATTG 810
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RESULT 7
BF264498 842 bp mRNA EST 09-MAR-2001
LOCUS HV_CEA0009709f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
ACCESSION BF264498
VERSION BF264498.2 GI:13261550
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 842)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Nov 17, 2000 this sequence version replaced gi:11195492.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCTACTAAAGG
High quality sequence stop: 604.
FEATURES
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/notes="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 189 a 255 c 255 g 143 t
ORIGIN

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Matches 596; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 172 gacgccttcacgcgcgcgcaacacottccggggttcggccaccacggcgccgac 231
Db 63 GAGCGCTTCATCGCGGAGCCACACACTTTCCGGGCTTCGGCACCCAGCGCGCGAT 122

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Db 183 ACGAGAGCGCGCGGACGACGATCCCAATGSGGCTACTGCTTCAAGGAAGAGATAAGCAAG 242
QY 352 gccagttccaccactactatgacgaggggagaccatccaattgacagggcggtccaactac 411
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QY 412 gatcttgcgggagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 471
Db 303 GATCTCGCGCGGAGAGCGATCGGGAAGGACCTGTGTAGCAACCCGGATCTGTGTCTCACT 362
QY 472 gacgggtgtgtctcttcagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 531
Db 363 GACGGGTTGTCTCTTCAGGACAGCGATGTGGTCTGGATGACGGCGCACGGCAACAG 422
QY 532 ccgtcgtgccacaagtcgcctcagccctgagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 591
Db 423 CGTGCAGGACCATCGTCTCGCTACGCCGCTGAGCGCGGACTGCCGGCGACACCGCTGCC 482
QY 592 ggcagggtaccgggatacagagtgatcaccaatataatcaacgagggcggtcagtgccgga 651
Db 483 GGTGCGGTTTCCAGGGTACCGGTGTAGCACCAATATCATCAACGGCGGGTCTGAGTGGGCG 542
QY 652 atgggcgcggaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 711
Db 543 ATGGGCGCGGAGGACGCCAACGTCGATCGCATCGGATCTACACGGCTACTTGGGGGATG 602
QY 712 ctgcggcgccaccggaggagcaacctgcactgactgtacacccagaggaaacttcg 763
Db 603 CTCGGGACGGGACCGGGGCAATCTTAAGTCTACACCAACAGGGGACGTTG 654

RESULT 8
BE215473 669 bp mRNA EST 09-MAR-2001
LOCUS HV_CEB0006009f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCDA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
ACCESSION BE215473
VERSION BE215473.2 GI:13264441
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 669)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Jul 3, 2000 this sequence version replaced gi:8903085.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCTACTAAAGG
High quality sequence stop: 644.
FEATURES
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/cultivar="C116151 (M1a6)"

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RESULT 10
LOCUS BE214283 725 bp mRNA EST 09-MAR-2001
DEFINITION HV_CEB0003A01f Hordeum vulgare seedling green leaf EST library
HV_CEB0003A01f (Erysiphe infected & control) Hordeum vulgare cDNA clone
ACCESSION BE214283
VERSION BE214283.1 GI:8901895
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 725)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 670.

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see http://www.genome.clemson.edu/projects/barley/ to
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 165 a 226 c 211 g 123 t
ORIGIN

Query Match 67.9%; Score 523.6; DB 10; Length 725;
Best Local Similarity 94.9%; Pred. No. 3.6e-91;
Matches 541; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 202 CCGGCTTCGGCACCACCGGCGCGGTGACATCAAGCGCGAGCTCGCGCTTCTC 261
Db 2 CCGGCTTCGGCACCACCGGCGCGGTGACATCAAGCGCGAGCTCGCGCTTCTC 61

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QY 262 ggcacagctccacagacacacgagagagagagagagagagagagagagagagagagag 321
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QY 322 ggtactgtctcaaggaagagataagcaagggcaccagctccccaccatactatggacggga 381
Db 122 GGTACTGTCTCAAGGAAGAGATAAGCAAGGCCACGCTCCACCTACTATGAGACGGGA 181
QY 382 cccatcaatgacagggcggtccaaactagatcttccgggagagagatcggaagagac 441
Db 182 CCCATCAATTGACAGGGCGGTCCACTAGATCTCCCGGGAGAGGATCGGGGAAGAC 241
QY 442 ctggtgagcaacccagacacctagtgtccacgagcggtgtgtctcttcagagagggccatg 501
Db 242 CTGTGAGCAACCGGATCTGTGTCCACGACGCGGTGTGTCTTTCAGGACGGCGATG 301
QY 502 tgttttgatgacggcgaggggaaacacgcccgtgtgcccacacgtgcgccctacgcgc 561
Db 302 TGGTTCCTGGATGACGGCGCAGGGCAACAAGCCGTCGAGCCACAACGTCGCCCTACGCCG 361
QY 562 tggacgcccagcgccgcgacacgcgtgcccggcaggggtaccggatagcgagtgatcacc 621
Db 362 TGGAGCGCGAGCGCGCGACACCGCTGCCGGTCCGGGTTCAGGCTACGGTGTAAATCACC 421
QY 622 aatatcatcaacggcggtcgagtcgagtcgggaatggcggaacgacgcaacgtgcgaccgc 681
Db 422 CATATCATCAACGGCGGCTCGAGTGGGATGGCGGGAACGACGCAACGTCATTCG 481
QY 682 atcgctactacagcctactcgccatctcgccacgacgacgacgacgacgacgacgacgac 741
Db 482 ATCGCTACTACAGCCGCTACTCGGCATGCTCGGCATGCTCGGCATGCTCGGCATGCTCGGC 541
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RESULT 11
BF628657
LOCUS BF628657 713 bp mRNA EST 21-FEB-2001
DEFINITION HVSMEB0006P01f Hordeum vulgare seedling shoot EST library
HVCDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone
HVSMEB0006P01f, mRNA sequence.
ACCESSION BF628657
VERSION BF628657.2 GI:13090309
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 713)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Dec 19, 2000 this sequence version replaced gi:11892815.
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 703.
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/cultivar="Morex"
FEATURES
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	/lab_host="TJC121"	
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	more details on library preparation and sequence analysis	
	see http://www.genome.clemson.edu/projects/barley/ To	
	order a clone see http://www.genome.clemson.edu/orders"	
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ORIGIN		
Query Match	66.4%; Score 511.6; DB 11; Length 713;	
Best Local Similarity	89.0%; Pred. No. 7.2e-89;	
Matches 564; Conservative 0; Mismatches 69; Indels 1; Gaps 1;		
QY 33	cgcgcgtctcgtcgccgtggcggcggggggtgccggcgcgagggcggtgggctcgggt 92	
Db 80	CGCGCGCTCCTGCTCTCCGTGGGGTGGCGGCCGCGGGCGCAAGCGTGCGCTCCGT 139	
QY 93	catcacggytggtgtacgcgagcaactctgccaaaccgcgcgaacaactcgtgtgcccggc 152	
Db 140	CATCACCAATTCGGAGTACGCAGCATGCTGCCAAGCGGCACAACTCGAGTCCGGGC 199	
QY 153	cagagggtttacacgttacacgccttcattcgcgcgcgcaccaacctcccggactcgg 212	
Db 200	CAGGGGGTTCTACAGTACAGCGCTTCATCGCCCGCCGCACACACTTCGGGGCTTCGG 259	
QY 213	cacacccggcagcgccgcacacatcaagcgcgaactcgcgcgcctttctcggcagaactc 272	
Db 260	CACCACCGGAGGAGATAACAAGCCACAGTCAAAGCGGAGCTCGCGCTCTCTCAGCGAGACTT 319	
QY 273	ccac-gagaccacgcgaggacagagagcgtgccgaccagtccagtgggctaactcgt 331	
Db 320	CCACTGAGACTACCGGAGGACGAGAGGGCGCGCGACCACTCCAATGGGGCTACTGCT 379	
QY 332	tcaaggaagatagaagaagccaagtcgccaccatactatggacggggagccccatccaat 391	
Db 380	TCAAGGAGGAGATAACAAGCCACAGTCTCCACCTACTATGAGCGGGGCCCATTCAT 439	
QY 392	tgacaggcggtccaaactacgatatttcggggagagcgatcggaagagacctggtagca 451	
Db 440	TGACAGGGCAGTCCAACTACATGATCTCTCCGGGAGGGCGATCGGGAAGACCTTTGTAGCA 499	
QY 452	accagacctagtgtaocaggaagcggtggtgtccttcaggacggcatactgggttcgga 511	
Db 500	ACCGGACCTGGTGTCCACAGCGCGTGGTGTCTTTCATACCGGCCATTGGTTCGGA 559	
QY 512	tgacycgagggaaaacaagccgtcgtgcacaaactcgcgcactacgcgcgtggacgga 571	
Db 560	TGACGGCTCAAGGCAACAAGCCGTGAGGCCAACACAGCGCCTATGCGCGCTGGACCGCA 619	
QY 572	cgcgcgcgcacacctgcgcggcaggggtacccgatatcgcggatagtgatcaccaaatatca 631	
Db 620	CAGTGC CGATACAACTG CAGGTGCGGTGCTGGATACCGCGTTATCACCAAAATTATA 679	
QY 632	acggcggttcgagtgcgggaatggcgccgaagca 665	
Db 680	ACAGCGGCTCCAAATGCGGATCGGCATAAGCAACGA 713	

RESULT	12
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LOCUS	
DEFINITION	BE216024 583 bp mRNA EST 09-MAR-2001 HV_CBD009C12f Hordeum vulgare seedling green leaf EST library HVCNNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV_CEB0009C12f, mRNA sequence.
ACCESSION	BE216024
VERSION	BE216024.1 GI:8903636
KEYWORDS	EST,
SOURCE	barley.

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 583)
AUTHORS Wing,R., Closer,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAGCCCTCACTAAAGGG
High quality sequence stop: 581.
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
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library HVCDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
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more details on library preparation and sequence analysis
see <http://www.genome.clemson.edu/projects/barley/> To
order a clone see <http://www.genome.clemson.edu/orders>"
BASE COUNT 108 a 191 c 189 g 94 t 1 others
ORIGIN

[illegible]

Db 549 GACGGCCCAAGGCAACAG 567

Search completed: May 3, 2002, 16:23:53
Job time: 7193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 15:34:10 ; Search time 3990.51 Seconds
(without alignments)
4018.348 Million cell updates/sec

Title: US-09-534-229c-7

Perfect score: 972

Sequence: 1 atctcacgcctgagagcg.....ttgggtcgcgacagtgta 972

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

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9: gb.pr.*

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12: gb.sy.*

13: gb.un.*

14: gb.yi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.om.*

20: em.or.*

21: em.ov.*

22: em.pat.*

23: em.ph.*

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25: em.ro.*

26: em.sts.*

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28: em.un.*

29: em.vi.*

30: em.htgo_hum.*

31: em.htgo_inv.*

32: em.htgo_rod.*

33: em.htg_hum.*

34: em.htg_inv.*

35: em.htg_rod.*

36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	590.8	60.8	1186	8	OSLMRNAC	X56787 O. sativa L.
2	569.6	58.6	1779	8	BLYCHI33A	L34211 Hordeum vul
3	567.8	58.4	1291	8	RICCHIT3A	L37289 Oryza sativ
4	561.2	57.7	1173	8	AF000965	AF000965 Poa prate
5	553.2	56.9	1080	8	AF000966	AF000966 Poa prate
6	543.4	55.9	1192	8	AF280437	AF280437 Secale ce
7	537.6	55.3	1051	8	OSD02286	U02286 Oryza sativ
8	537.4	55.3	1985	8	TACHIG	X76041 T.aestivum
9	536.4	55.2	1684	8	HV002287	U02287 Hordeum vul
10	536	55.1	1191	8	AB051578	AB051578 Secale ce
11	519.6	53.5	1252	8	AF000964	AF000964 Poa prate
12	518.4	53.3	2808	8	RICCHT3	D16223 Rice Cht-3
13	518.4	53.3	141534	2	AP003685	AP003685 Oryza sat
14	500.6	51.5	2739	8	RICCHT1	D16221 Rice Cht-1
15	496.6	51.1	1151	6	I84465	I84465 Sequence 2
16	490.6	50.5	1160	8	XSEND0	X56063 O.sativa mR
17	481.6	49.5	1237	8	OSCHIT	X54367 Oryza sativ
18	474.6	48.8	1159	8	OSCHITIA	Z29961 O.sativa (P
19	473.4	48.7	2048	8	OSDNARC24	X87109 O.sativa (P
20	469.4	48.3	998	8	BLYCHI	M62804 H.vulgare L
21	469.4	48.3	1002	6	A37990	A37990 Sequence 9
22	469.4	48.3	1002	6	AR037574	AR037574 Sequence
23	469.4	48.3	1002	6	I75200	I75200 Sequence 9
24	469.4	48.3	3169	8	BLYCHI26A	L34210 Hordeum vul
25	455	46.8	1018	8	AB051579	AB051579 Secale ce
26	450.8	46.4	2986	8	RICCHT2	D16222 Rice Cht-2
27	416.2	42.8	1280	8	AB018248	AB018248 Oryza sat
28	416.2	42.8	1300	8	AB012855	AB012855 Oryza sat
29	412.8	42.5	1120	8	PACHII	Z78202 Persea amer
30	407.4	41.9	1132	8	PHVCHM	M13968 P.vulgaris
31	405.4	41.7	892	8	AF307511	AF307511 Vigna ses
32	402.2	41.4	1146	8	VURNACHI1	X88800 V.unguicula
33	397.6	40.9	1100	8	OSCHITIB	Z29962 O.sativa (P
34	397.2	40.9	1128	8	MZECHITC	L00973 Zea mays ac
35	396.2	40.8	4704	8	S43926	S43926 CHSB-chitin
36	382.6	39.4	1058	8	AB015655	AB015655 Cucurbita
37	379.6	39.1	1070	8	AB048531	AB048531 Psophocar
38	375	38.6	879	6	E13289	E13289 cDNA encodi
39	375	38.6	998	6	E13290	E13290 cDNA encodi
40	371.6	38.2	1225	6	I23881	I23881 Sequence 1
41	371.6	38.2	1225	6	I92331	I92331 Sequence 1
42	369	38.0	1012	8	MZECHITINA	L16798 Zea mays cl
43	367.6	37.8	1007	8	ALCCHINTIA	M94106 Allium sati
44	366.8	37.7	1670	8	PEACHIT2I	L37876 Pisum sativ
45	354.6	36.5	888	8	HBR238579	AJ238579 Hevea bra

ALIGNMENTS

RESULT 1

OSLMRNAC	OSLMRNAC	1186 bp	mRNA	PLN	05-MAY-1995
LOCUS	O.sativa L. mRNA for endochitinase.				
DEFINITION	X56787				
ACCESSION	X56787.1	GI:407471			
VERSION	endochitinase.				
KEYWORDS	Oryza sativa.				
SOURCE	Oryza sativa.				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1 (bases 1 to 1186)				
AUTHORS	Nishizawa, Y., Kishimoto, N., Saito, A. and Hibi, T.				
TITLE	Sequence variation, differential expression and chromosomal location of rice chitinase genes				
JOURNAL	Mol. Gen. Genet. 241 (1-2), 1-10 (1993)				
MEDLINE	94049667				
REFERENCE	2 (bases 1 to 1186)				
AUTHORS	Nishizawa, Y.				

TITLE Direct Submission
JOURNAL Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
305, JAPAN

FEATURES
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/db_xref="taxon:4530"
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10..1032
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ORIGIN

Query Match 60.8%; Score 590.8; DB 8; Length 1186;
Best Local Similarity 77.1%; Pred. No. 1.2e-71;
Matches 743; Conservative 0; Mismatches 197; Indels 24; Gaps 1;

QY 25 gcaagcgctcctgcgcgtcgtctgctgagcgccgagcgccggtcagccgagcgccagcgccag 84
DB 49 GCGGCGCTGTGGCGCTGGCGCTGCTGGCGCGCGCTGCGAGCGCGCGCGCGCGAG 108

QY 85 cagtgcggtcgcgaagcgccgagcgccgagcgccgagcgccgagcgccgagcgccagtcgac 144
DB 109 CAGTGGCGCGCAGCG 168

QY 145 ggtttctgcggaccactccgactcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 204
DB 169 GGTGTGTGCGCGCACCTCCGCTTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 228

QY 205 tgcgg-----tgccgagcgccgagcgccgagcgccgagcgccgagcgccagtcgac 240
DB 229 TCGGCGCGCAGCG 288

QY 241 tccagggacctcttcagcggttctgctccatcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
DB 289 CCCAGGCGACCTGTTCGAGCGGCTCTCTCCACCGCAACGACGCGGCGGTGCCCGCGCGC 348

QY 301 ggtttctacagtaacagcgttctgctccgagcgccgagcgccgagcgccagtcgac 360
DB 349 GGTGTGTACACCTACAGGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408

QY 361 accggagacctgacacgcggaagcgagcggtgagcgcttcttcggccagacctcac 420
DB 409 ACCGGCACACGACG 468

QY 421 gagaccacggcggttgccaccgagcgccgagcgccgagcgccgagcgccgagcgccgagcgcc 480

Db 469 GAGACACCGCGGCTGCG 528

QY 481 aagcagagcagggctgc 540

Db 529 AAGCAGGAGCAGAACCCGCGCTGCGACTACTGCGAGCGCTCGCGGAGTGCGCGCGTGGCG 588

QY 541 cccggcagcagctactatggc 600

Db 589 CCCGCGCCAGTACTAGCG 648

QY 601 ccgcgccgc 660

Db 649 CCGCGCGGAGGCGATCGGGGTGGACCTGCTGAGCAACCGGACCTGGTGGCGACGCGAC 708

QY 661 ccgacagtggcgttcaagagcgagc 720

Db 709 GCGAGGCTGTCTCAAGACGCGCGCTGTGGTTCGTGGATGAGCGCGCGAGGCGGGAACAACG 768

QY 721 tcgtgccatgacgtgacgc 780

Db 769 TCGAGCCACGACGATGATCAGCGGCGCGGTGGCGCGCTCGCGCGCGCGCGCGCGCGCG 828

QY 781 cgggtacccgggtatggtgttcacccacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 840

Db 829 CCGCGCGCGGCGGTACGGCGCTGATCACCACATCGTCAACGCGCGCGCTGGAGTGGCGGCG 888

QY 841 ggcgcagacacaaagtgccgagc 900

Db 889 GCGCGCGACGACCGCGGTGGCGACCGGATCGGCTTCTACCGCGCGCGGTTCACAGCGCG 948

QY 901 ggc 960

Db 949 GGCATCGCGCGCGCGCGCAACCTCGACTGCTACACCGAGCGCGGTTCACAGCGCGCGTCG 1008

QY 961 gcgg 964

Db 1009 TCGG 1012

RESULT 2
LOCUS BLYCHI33A
DEFINITION Hordeum vulgare chitinase (CHI33) gene, complete cds.
ACCESSION L34211
VERSION L34211.1 GI:576566
KEYWORDS chitinase.
SOURCE Hordeum vulgare seed DNA.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1779)
AUTHORS Leah,R.; Skriver,K.; Knudsen,S., Ruud-Hansen,J., Raikhel,N.V. and Mundy,J.
TITLE Identification of an enhancer/silencer sequence directing the
aleurone-specific expression of a barley chitinase gene
JOURNAL Plant J. 6, 579-589 (1994)
MEDLINE 95078949
COMMENT On Nov 28, 1994 this sequence version replaced gi:507960.
FEATURES
source Location/Qualifiers
1..1779
/organism="Hordeum vulgare"
/db_xref="taxon:4513"
/tissue_type="seed"
614..620
682..1680
/gene="CHI33"
/gene="CHI33"
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/codon_start=1
/function="hydrolysis of chitin"
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TATA_signal
gene

CDS

D	b	1537	GSGGCGAGACGGCTGTGCCGACGGATCGGCTTCTACCAGCGCTACTGCACATCCTT	1596
Q	y	901	ggcatcggtacggaataaacctcgaactgcctacaccaeatttgttcaagttgggctc	960
D	b	1597	GSCGTGGGTACGGGGGCAACCTCGACTGCTACACACAGAGCGCCCTTCGTCAGGGGCTT	1656
Q	y	961	ggggcacagtga	972
D	b	1657	CTCATTTTCAGCGA	1668

[illegible]


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QY 739 acggggtgactccgacggccagagtagcgcagccgagcggttacccgggtatggt 798
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Db 935 ACCGGCAGTGGAGCCCTCGGGCGCAGACCAGCGGGGGAGGTTCCTCGGTACGGC 994

QY 799 gtcataccaacgctacaaagcgaggatccaatgcggatcggtgggagacgacaagtgtg 858
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Db 995 GTGATCACTAATCATCAACAGCGGGGCTCGAGTCGCGCAAGGGGCGAGACAACGGGTC 1054

QY 859 gcgtagcgatcggtttctcaagcgctattgtacattttcgcatcgctacggaat 918
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Db 1055 GCCACAGGATCGGGTCTTACAGCGTACTTCGACCTCTCTCGGCGTACGCTACGGGAC 1114

QY 919 aacctgactgtctaaacaaattgtcttcaacgtt 954
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Db 1115 AACCTGGACTGCTACAACAGGAGCGCTTCAATGGT 1150

RESULT 5
AF000966 AF000966 1080 bp DNA PLN 31-OCT-1999
LOCUS Poa pratensis chitinase (Chi2) gene, complete cds.
DEFINITION Poa pratensis chitinase (Chi2) gene, complete cds.
ACCESSION AF000966
VERSION AF000966.1 GI:6164587
KEYWORDS Kentucky bluegrass.
SOURCE Poa pratensis
ORGANISM Poa pratensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poae; Poa.
REFERENCE 1 (bases 1 to 1080)
AUTHORS Du,M. and Ha,S.B.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley, CA
94706, USA
FEATURES
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                        VATDPIVSKTALWFMTAOSPSPSHAVITGQWSPSADQAAAGRPVPGYVITNINL
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BASE COUNT 208 a 366 c 327 g 179 t
ORIGIN
Query Match 56.9%; Score 553.2; DB 8; Length 1080;
Best Local Similarity 75.6%; Pred. No. 1.6e-66;
Matches 712; Conservative 0; Mismatches 203; Indels 27; Gaps 1;

QY 34 gtcctgaccgtcgtctggcgccgagcgcggtcagcgccagcgccagcgagcagtcggc 93
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Db 40 GTGGTGTGACCATTCGTGTCGGCGCCTTCGCCGTGCTGCACACGCGGACGTGCGGC 99

QY 94 tcgcaagcggcgccgagcgcaagtgcgcgaactgctgtgctgacgacagtcggtctcgc 153
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Db 100 TCGCAGCGCGGGGGACGTGCCCAACTGCTCTGCTGCACCAATTCGGTTCGCG 159

QY 154 ggcacacactccgactactgcggcccgctgcccagagcgaagtcagtcggtgag- 212
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 GGCACACACTCCGACTACTGCGGACCGGCTGCCAGACGCCAGTGCACAGCGCTGCAGCGGC 219

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QY 213 -----cgggcgggcggggtggcctccatcgtgtccagg 246
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Db 220 CCCACGCGGGTGAACCCGACTCCCTCCGGCGCGCGCGGTCTCTCCATCGTATCTCAG 279

QY 247 gacctcttgagcggttctctctccatcgcaacgacgagcgtgctggcccggggttc 306
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Db 280 TCGCTCTTCGAGCAGATGCTTCTGACCGCAACGACGCGGATGCTGTGGCCAAAGGGTTTC 339

QY 307 tacaagtacgacgctcttgccgcgccgcgcggttcccggttcgggacacacggga 366
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Db 340 TACACCTACAAACGGCTTCATCGCGCGCGCCAACTCTTTGCGCGGTTTCGGGACACCGGGC 399

QY 367 gacctggacacgcggaagcgaggtggtggcgcttcttcggccagacctctcacagacc 426
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Db 400 AGCACCGAGGTCAGGAAGCGGAGGTGGCGCGCTTCCTCGCTCAGACCTCCACAGAGACC 459

QY 427 accggcggtggccacgcgcgcgcgcgccttctctatggggtcactgcttcaagcag 486
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Db 460 ACCGGCGGGTGGCGGAGCGCGCCATCCAGATCTCTTACAACACTACAACACGCGGCGCAG 519

QY 487 gagcagggctgcgcgcgagctactgcgacgacgagcgcgactgcccgtgcgacccggc 546
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 GAGCAAGGGCCACTCTCGGACTACTGCTCGCGGAGCTCGAGTGGCGGTGGCGCGCGGG 579

QY 547 aagcagtactatggccggggcccatccagctcaccacaaactacaactacgacggcgcg 606
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Db 580 AAGAAGTACTTCGGCGGGGCGCCATCCAGATCTCTTACAACACTACAACACGCGGCGCAG 639

QY 507 ggcgcgcaatcggggtggacctgtgaacaaatcggacctggtggccacgagccgaca 666
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Db 640 GGACAGGCCATCCAAACTGACTGCTCAACAAACCGGACCTTTGGGCCACAGACCGGACC 699

QY 667 gtgcgttcaagacggcgatggtctgtgatgacgacgagtcacaaagccgtcgtgc 726
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Db 700 GTGTCGTCAAGACGCGCTGTGTTCTGTGATGACGGCTCAGTCGCCCAACGCGTCGAGC 759

QY 727 catgactgatacggggctgtgacctccgacggccggggtatagcagccggacgggta 786
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QY 787 ccgggtatggtgtcatcaccacgctcatcaacggcgagtcacatcgccatcgccatgggacg 846
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Db 820 CCCGGTACGGCGTGATCACCAACATCATCAATGCGGGCTCGAGTGGGGAAGGCGAG 879

QY 847 aacgacaaggtggcgatcgatcggtgttctacaagcgctattgtgacattttcgcatc 906
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Db 880 GACAACCGCTCGCAGACCGGATCGGGTTCTTACAAGCGCTACTCGGACCTCCTCGGGCTC 939

QY 907 ggtacgggaataacctgactgtataacaaattgtcgttc 948
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Db 940 AGCTACGGAAACACCTGGACTGCTACAGCCAGCGGCGGTTTC 981

RESULT 6
AF280437 AF280437 1192 bp mRNA PLN 12-FEB-2001
LOCUS Secale cereale 31.7 kDa class I endochitinase-antifreeze protein
DEFINITION Secale cereale 31.7 kDa class I endochitinase-antifreeze protein
precursor, mRNA, complete cds.
ACCESSION AF280437
VERSION AF280437.1 GI:12407646
KEYWORDS
SOURCE rye.
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
Secale.
REFERENCE 1 (bases 1 to 1192)
AUTHORS Yeh,S., Moffatt,B., Griffith,M., Xiong,F., Yang,D.S.C.,
Wiseman,S.B., Sarhan,E., Danyluk,J., Xue,Y.Q., Hew,C.L.,
Doherty-Kirby,A. and Lajoie,G.
TITLE Chitinase genes responsive to cold encode antifreeze proteins in
winter cereals

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Db	884	GACACGCGCTGGCAAAACCGGATCGGCTTCTACCAAGCGCTACTCGGCGCGGCTCGGCATC	943
QY	907	ggctacgggaataaactgcactgcatacaacaattgtcgttcaacggttggtcgcg	964
Db	944	GGACCGCGGCAACCTCGACTGCTACACACAGAGCGGCTTCAACAGCGGCTCGTCGG	1001
RESULT	8		
TACHIG			
LOCUS	TACHIG	1985 bp	DNA
DEFINITION	T.aestivum (Chinese spring)	chi gene for endochitinase.	
ACCESSION	X76041		
VERSION	X76041.1	GI:416028	
KEYWORDS	CHI gene; endochitinase.		
SOURCE	bread wheat.		
ORGANISM	Triticum aestivum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.		
AUTHORS	Liao, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH, Worringen Weg, 52056 Aachen, FRG		
REFERENCE	2 (bases 1 to 1985)		
AUTHORS	Liao, Y.C., Kreuzaler, F., Fischer, R., Reisner, H.J. and Tiburzy, R.		
TITLE	Characterization of a wheat class Ib chitinase gene differentially induced in isogenic lines by infection with Puccinia graminis		
JOURNAL	Plant Sci. 103, 177-187 (1994)		
FEATURES	Location/Qualifiers		
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GC_signal	/gene="CHI"		
	71..75		
GC_signal	/gene="CHI"		
	250..254		
CAAT_signal	/gene="CHI"		
	390..394		
TATA_signal	/gene="CHI"		
	529..536		
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	600..>1595		
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	633..1595		
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BASE COUNT	467 a	554 c	552 g
ORIGIN	412 t		
Query Match	55.3%	Score 537.4;	DB 8; Length 1985;
Best Local Similarity	74.5%	Pred. No. 1.7e-64;	
Matches 704;	Conservative	0; Mismatches	211; Indels 30; Gaps 1;


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/protein_id="BAB18519.1"
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NGNIEGCHGQSDRADIRIGFYKRYCDILRVYGNLDCYNQRPEFA"
BASE COUNT      236 a   382 c   355 g   218 t
ORIGIN
Query Match      55.1%; Score 536; DB 8; Length 1191;
Best Local Similarity 74.3%; Pred. No. 3.3e-84;
Matches 708; Conservative 0; Mismatches 210; Indels 36; Gaps 1;
QY      31  gcgctctggcgcgtctcctggcgcgcgcggtcacgcgcgcgcgcgcagtcgc 90
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64  GCGTTCGCGTGTGTTCCGCTGCITGCCATGCGGGTGACCATGCCGTGCCGAGCATGC 123
QY      91  ggcctgaagcgcgcgcgcgcgcgcagtgogcgcgaatgcctgtctgcagccagttc 150
Ddb      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
124  GGCTCAGCGCGCGGGCGAGCTGCCCAACTGCCTCTGCTCAGCGCGTTCCGGTGG 183
QY      151  tgcggcaccactccgaactactcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 210
Ddb      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
184  TGGGGTCCACTCTCGACTACTTGGGGCAGCGGATGCCAGACGACAGTGTGCGCGGTGCGGC 243
QY      211  ggc-----ggcgcgcggggtggcctcc 234
Ddb      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
244  GGGGCGCGCAGCGCGCTCACTCCACGCCACCCCATCGGGCGCGCGGTCTCCTCC 303
QY      235  atcgctcagggaacctcttcgagcgttccctcactcgcacgcgcgcgcgcgcgcgcgc 294
Ddb      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304  ATCGTTCGGCGCGCCTCTTCGACCGGATCGTGTGCACCGAGGTGCGCGCTTCGCGCAG 363
QY      295  gccgcgggtttcacgtacgcgcgccttttgccgcgcgcgcgcgcgcgcgcgcgcgcgc 354
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364  GCCAAGGGCTTCTACACCTACGACGCGCTTCGTCGCGCGCGCGCGCGCTTCOCGGGCTC 423
QY      355  ggcacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 414
Ddb      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
424  GGCACCGCGGCGAGCAGCAGACCCGGAGCGGAGGTGCGCGCTTCGTCGCGCCAGCC 483
QY      415  tctcacgagaccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 474
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484  TCCACAGACACCGCGCGGTGGCGACGCGCGCGAGCGGCTTCGCTGCGGTGGGTAC 543
QY      475  tgcctcaagcaggagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 534
Ddb      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
544  TGCCTCAAGCAGGAGCGTGGCGCACCTTCCAACTACTGCACTCCACGGCGCAATGCCG 603
QY      535  tgcgcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 594
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QY      595  taaggaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 654
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664  TACGGGCCCGCGCGCGGCGCATTTGGGTGCGATCTGTGCGCAACCCAGACCTGTTGGCC 723
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724  ACGGACCCGACGGTGTGGTTTAGACAGCCATGTGGTGTGGATGACGGCACAGCGGCCA 783
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784  AAGCCGTGAGCCATCTGTGATCAGGGCGCTAGTGGAGCCATCAGGACCGACCGGGCT 843
QY      775  gcggcaggggtaccggggtatgtgtcatcaccacgaagtcatcaacgcgcgcgcgcgcgcgc 834
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844  GAGGCGGGGTGCCGGGTTTGGCGTGATCACCACATCGTCAATGCGGGATCGAGTGC 903

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Phone: 0298-38-7451
Fax: 0298-38-7408
Location/Qualifiers
1. .2808
/organism="Oryza sativa"
/strain="Nipponbare"
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1723. .1730
1733
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FEATURES

source

TATA_signal

misc_feature

CDS

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BASE COUNT 697 a 737 c 708 g 666 t
ORIGIN Chromosome 6.

Query Match 53.3%; Score 518.4; DB 8; Length 2808;

Best Local Similarity 73.0%; Pred. No. 5.5e-62;

Matches 707; Conservative 0; Mismatches 231; Indels 30; Gaps 2;

QY 11 tgaagagcgggtgtcagcggcgtctcggcgtgtcctggcggcgccgcgggtcagc 70

Db 1816 TCACATTGCGGCGCCCGATGAGAGCTCTCGCTCTCGCGGTGTGCGCCATGCGCGGTGGT 1875

QY 71 cggccacggcgagcagtcggtcgcgaagcggcgccgcaagtgccgcgactgcctgt 130

Db 1876 CCGTGCAGGAGAGTGGCGGACCGAGCGGGCGCGCTCTGCGCCCACTGCCCTCT 1935

QY 131 gctcagcagcttgggtttcgggcacacactcgcactactcggcccccgcgtccaga 190

Db 1936 GCTGAGCAGTACGCTGGTGGCGCTCCACTCCGATTACTGCGCGCGCGCTGCCAGA 1995

QY 191 gccactgcactgctgcgtgagc-----ggcgcgcgcg 223

Db 1996 GCCATGCTTCGGCGGCTGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2055

QY 224 ggggtgcctccatcgtgtccaggagccttcttcgagcgttctcgtccatcgcacagc 283

Db 2056 GCGTGCCTCCATCATATCGCCCTGCTCTTCGACCAATGCTGCTCCACCGCAACGACC 2115

QY 284 cagcgtgctggccgcgggtttctacacgtacgacgaccttctggccgcggcgcgct 343

Db 2116 AGGCGTGGCGCGCTTAAGGCTCTTACACTAGACGCTTCTGTCGCGCGCGCGCGCGCT 2175

QY 344 tccggccttcggcaccacggagacacctggaacgcgggaagggagtgcgccctct 403

Db 2176 ACCCGGACTTCGCCACCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 2235

QY 404 tcggccagacctctcagacaccacggcggttgcccccacgcgcgcgcgcgcctct 463

Db 2236 TGGCGCAGACGTCGCCACGAGACCACCGCGGCTGGCCACACGCGGCCGACGCGCCCTACT 2295

QY 464 catgggctactgcttcaagcagag---cagggtcgcgcggagctactcgcaccaga 520

Db 2296 CTGGGGCTACTGCTTCAAGGAGGAGAACACGCGCAACGCCCCACATACTCGGAGCCCA 2355

QY 521 ggcgcgactggcgtgcaccccgaagcagctactatggcgcggcccccattccagctca 580

Db 2356 AGCGGAGTGGCGGTGCGCGCGGCAAGAGTACTACGCGCGGGGACCCATCCAGATCA 2415

QY 581 ccacacatacaatacagcagcggcgccgcgcaatcgggggtgacctgtgtaacaatc 640

Db 2416 CTTAACTACAACTACGCGCGCGGCGGCGAGGCATCGGCTCCGACCTGTCTCAACAACC 2475

QY 641 cggacctggtggccacggaccgcagcagtggggttcaagacggcgatggttcttgatga 700

Db 2476 CGGACTGGTGGCTCGGACGCCACCGTCTCTTCAAGACGCGTCTGTTCTGGATGA 2535

QY 701 cgaacgagtcacacaaagcgtgctgccaatgacgtgacacgggggtggaactccgacgg 760

Db 2536 CGCGCAGTCGCCCCAAGCGCTGTCACCGCGGTGATCACCGGCCAGTGGACGCCGCTCCG 2595

QY 761 ccagggtatagcgacgcggcaggggtaccgggtatgggtgtatcaatacaacacgtcaacag 820

Db 2596 CCGACGACGAGCGCGCGGCGCTTCCGGGCTACGGCGAGATCACCAACATCATCAACG 2655

QY 821 gggggtacaaatggcgcatggggcagacacaaagtggtggcgatcggtcggttcttaca 880

Db 2656 GCGGTGTGAGTGGCGGCGCACGCGCGGACGACAAAGTGGCGGACCGGATCGGTTCTACA 2715

QY 881 agcgtattgtgaacttttcggatcggtacgggaataaacctgaactgtacaaccaat 940

Db 2716 ACGCTACTGCGACATGCTGGCGCTCAGCTATGGCGATACCTGGATTGCTACAACCCAGA 2775

QY 941 tctgcttc 948

Db 2776 G3CCCTAC 2783

RESULT 13

AP003685/c

LOCUS

DEFINITION

AP003685.1

ORYZA SATIVA CHROMOSOME 6 CLONE P0548E04, *** SEQUENCING IN

PROGRESS ***

HTG

HTGS PHASE2

ORYZA SATIVA

ORYZA SATIVA

1 (sites)

Sasaki, T., Matsumoto, T. and Yamamoto, K.

ORYZA SATIVA NIPPONBARE(GA3) GENOMIC DNA, CHROMOSOME 6, PAC

CLONE:P0548E04

Published Only in Database (2001) In press

2 (bases 1 to 141534)

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (23-MAY-2001) Takuji Sasaki, National Institute of

Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail: tsasaki@abrr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/)

Tel: 81-298-38-7441, Fax: 81-298-38-7468

NOTE: It currently consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces is believed

to be correct as given, however the sizes of the gaps between them

are based on estimates that have provided by the submitter. This

sequence will be replaced by the finished sequence as soon as it is

available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

ORYZA SATIVA CHROMOSOME 6 CLONE P0548E04, *** SEQUENCING IN
PROGRESS ***
HTG
HTGS PHASE2
ORYZA SATIVA
ORYZA SATIVA
1 (sites)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
ORYZA SATIVA NIPPONBARE(GA3) GENOMIC DNA, CHROMOSOME 6, PAC
CLONE:P0548E04
Published Only in Database (2001) In press
2 (bases 1 to 141534)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
Submitted (23-MAY-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@abrr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/)
Tel: 81-298-38-7441, Fax: 81-298-38-7468
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:32:02 : Search time 309.71 Seconds
(without alignments)
2690.647 Million cell updates/sec

Title: us-09-534-229c-7
Perfect score: 972
Sequence: 1 atgtcacgctgagagcgcg.....ttgggtcgcgcgcacagtga 972

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_1101.*

- 1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.4	55.9	954	AA24889	Rye chitinase-like
2	496.6	51.1	1151	AAQ31408	RCH10 chitinase ge
3	496.6	51.1	1151	AAQ81346	Rice chitinase RCH
4	496.6	51.1	3035	AAAF54983	Nucleotide sequenc
5	493.4	50.8	1163	AAAF54983	CDNA encoding a ma
6	469.4	48.3	1002	AAQ62518	Sequence encoding
7	416.2	42.8	1318	AAV49982	Floral organ-speci
8	396.2	40.8	4704	AAQ05264	Sequence encoding
9	375	38.6	879	AAAT79940	Chitinase coding s
10	375	38.6	998	AAAT79941	Full length chitin
11	370	38.1	1225	AAAT33325	American elm chiti

12	337.6	34.7	7397	20	AA235613	Banana ripening fr
13	316.8	32.6	1152	12	AAQ12898	Tobacco intracellu
14	316.8	32.6	1152	18	AAAT89952	Nicotiana sp. intr
15	316.8	32.6	1152	21	AAAF58910	cDNA sequence enco
16	304.2	31.3	756	20	AA24890	Rye chitinase-like
17	297	30.6	721	20	AAV69461	Banana fruit ripen
18	296.4	30.5	1118	21	AAAF6233	CDNA encoding a ma
19	289	29.7	755	20	AAV69463	Banana fruit ripen
20	285.4	29.4	802	20	AAV69462	Banana fruit ripen
21	278.6	28.7	1013	21	AAAF6231	CDNA encoding a ma
22	277	28.5	1077	21	AAAF6230	CDNA encoding a ma
23	265.2	27.3	583	21	AAAF6234	CDNA encoding a ma
24	238	24.5	769	20	AAV69464	Banana fruit ripen
25	226.2	23.3	768	20	AAV69466	Banana fruit ripen
26	205.2	21.1	991	21	AAAF1918	Arabidopsis thalia
27	196	20.2	1010	11	AAQ06185	PR-Q cDNA cloned i
28	196	20.2	1020	10	AAAF0845	Tobacco PR-Q gene.
29	196	20.2	1020	20	AAV62809	Tobacco PR-Q gene
30	196	20.2	1020	20	AAV72995	PR-Q protein encod
31	192.6	19.8	2636	19	AAV49983	Floral organ-speci
32	186	19.1	1619	21	AAAF6227	CDNA encoding a ma
33	185.6	19.1	1317	21	AAZ48613	Nettle lectin cDNA
34	185.6	19.1	1317	22	AAQ60211	Urtica dioica aggl
35	183	18.8	965	12	AAQ12897	Petunia extracellu
36	183	18.8	966	18	AAAT8951	Petunia hybrida ex
37	183	18.8	966	21	AAAF58909	CDNA sequence enco
38	176.8	18.2	730	20	AAV69465	Banana fruit ripen
39	175.2	18.0	968	11	AAQ06186	PR-P cDNA cloned i
40	175.2	18.0	968	20	AAQ62813	Tobacco PR-P gene
41	175.2	18.0	968	20	AAV81601	PR-P protein encod
42	166.4	17.1	1116	21	AAAF6237	CDNA encoding a ma
43	163.2	16.8	1048	21	AAAF6232	CDNA encoding a ma
44	161.6	16.6	1153	13	AAQ21007	Sequence encoding
45	161.6	16.6	1153	15	AAQ68352	Endochitinase prec

ALIGNMENTS

RESULT	1
AA24889	
ID	AA24889 standard; cDNA; 954 BP.
XX	
AC	AA24889;
XX	
DT	21-JUN-1999 (first entry)
XX	
DE	Rye chitinase-like protein CHT9 cDNA clone ch-9.
XX	
KW	CHT9; chitinase-like protein; antifreeze protein; AFP;
KW	winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW	transgenic plant; preservation; cryopreservation; tumour; therapy;
ss.	
XX	
OS	Secale cereale.
XX	
FH	Key Location/Qualifiers
CDS	1..954
FT	/*tag= a
FT	/note= "separately claimed in Claim 2"
FT	
FT	sig_peptide 1..60
FT	/*tag= a
FT	mat_peptide 61..954
FT	/*tag= b
FT	/note= "separately claimed in Claim 2"
XX	
PN	WO9906565-A2.
XX	
PD	11-FEB-1999.
XX	
PF	31-JUL-1998; 98WO-CA00745.
XX	
PR	31-JUL-1997; 97US-0903872.

[illegible]

XX	Full length chitinase coding sequence.
XX	
XX	Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase;
KW	fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss
XX	
XX	Cucurbita pepo.
OS	
XX	
XX	Key Location/Qualifiers
FH	1.879
FT	/*tag= a
FT	/product= chitinase
FT	
XX	
PN	JP09163987-A.
XX	
XX	24-JUN-1997.
PD	
XX	
XX	14-DEC-1995; 95JP-0347367.
PF	
XX	
PR	14-DEC-1995; 95JP-0347367.
XX	
XX	(NIHA) JAPAN ENERGY CORP.
PA	(SEKI-) ZH SEKIYU SANGYO KASSETKA CENTER.
PA	
XX	
XX	WPI: 1997-380170/35.
DR	P-PSDB; AAW24554.
DR	
XX	
XX	Chitinase derived from pumpkin - used to protect plants against
PT	pathogenic fungi
PT	
XX	
PS	Claim 3; Page 4-5; 36pp; Japanese.
XX	
XX	This sequence represents the coding sequence for the pumpkin chitinase.
CC	Chitinase is an enzyme decomposing chitin (not present in plant cell
CC	membranes) found in the cell membranes of fungi. Plants have this enzyme
CC	to protect themselves from pathogenic fungi. Thus this enzyme can be use
CC	to prevent plants from being infected with pathogenic fungi, and the
CC	chitinase gene can be introduced into plants to improve their resistance
CC	to diseases caused by fungi. As the amino acid sequence of the chitinase
CC	does not have any region to be cleaved by ubiquitous peptidases in cells
CC	the chitinase produced by genetic recombination technology works for
CC	various host cells and serves for plant immunity to confer disease
CC	resistance on plants as the host.
XX	
SQ	Sequence 998 BP; 269 A; 238 C; 258 G; 233 T; 0 other;

Query Match	38.6%;	Score 375;	DB 18;	Length 998;
Best Local Similarity	65.9%;	Pred. No. 4.9e-57;		
Matches 581; Conservative	0;	Mismatches 285;	Indels	Gaps

Query Match	38.6%	Score 375;	DB 18;	Length 998;
Best Local Similarity	65.9%;	Pred. No. 4.9e-57;		
Matches 581;	Conservative 0;	Mismatches 285;	Indels 15;	Gaps
QY 82	gacagtgcgctctgcgaagcggcgggcgccaagtgcggccgaactgcctgtctgcagccag	141		
Db				
1	gagcaatgtggcggcagcgcaatggcgctctctgcgccaatgcctctgtcgcagccag	60		
QY 142	ttcgggttctgcggcaccactcgcgaactactgcggccccgcgtgcagagccagtgcc---	198		
Db				
61	ttcgggtggtcggcgaacccgcagcagtagtctgtaaaacaattgccagagccagtgcaaa	120		
QY 199	-----actggctgcgttgccggcgccggcggggtggcctccatcgtgtccagggac	249		
Db				
121	cccccagttaccggcgggcgccggcgccgagcgttggaagtatcatcaacgaagcc	180		
QY 250	ctcttcgagcggttctgtcccatcgcaacgcgcagcgtgcgctgccgcgggtctctac	309		
Db				
181	ctttacaataaagtctcaagtatacgaagtatcctcga tgcgccagtaatggattctat	240		
QY 310	acgtacgacgcctcttggccgcgcgcggcgcttcocggccttcggcacccgcgagac	369		
Db				
241	agatacaagtcttctactgcgcgtcctaactctctctgtgtttgtaccaccgcggagat	300		
QY 370	ctggcacgcgggaagcgggaggtggcgggcctcttcggccagaccctctcacgagacacc	429		

Db 736 tcaaaacggccttatggtctggatgacccacagtcaccagaagccctggtgcoatgac 795
 QY 733 gtgatacggggctgtgactcgcagcggccaggatagcgcagcggagcgggtaccggg 792
 Db 796 gtcatacgggaagtggagtccttcgcgaaccgacagtcgcggcggcgggttgcgggc 855
 QY 793 tatgtgttcatacacaacgctcacaacgctcgggagtcacatgcggtgagcgcagacgac 852
 Db 856 tacggcgtgatcacaacattatcaacgctgggagataatgcgggaaggttcaggttct 915
 QY 853 aaggtggcgatcgatcggtgtctacaagcgtattgtgacatttggcatcggtac 912
 Db 916 caagtggtggatcggtgattgattctacaagagtgactgtgatctctagagttgctat 975
 QY 913 gggataaactcgaactgctacacaacaaattgtcttcaacgtttgggtc 960
 Db 976 gggacaactctgattgctataacagagccttttgggaatgcactc 1023

RESULT 12

AAK25613

ID AAK25613 standard; DNA; 7397 BP.

XX AC

XX AC

XX AC

XX DT

XX XX

XX XX

XX DE

XX XX

XX KW

XX KW

XX KW

XX XX

XX OS

XX XX

XX PN

XX XX

XX PD

XX PF

XX XX

XX PR

XX PA

XX PI

XX XX

XX DR

XX DR

XX PT

XX XX

XX PS

XX XX

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

Query Match 34.7%; Score 337.6; DB 20; Length 7397;
 Best Local Similarity 61.5%; Pred. No. 1.4e-50;
 Matches 626; Conservative 0; Mismatches 302; Indels 90; Gaps 4;
 QY 20 ggtgtgcgacggcgtctcctggccgtgtgtcctggcgcgccgggtcagccggcagcg 79
 Db 5396 ggaggtatgaagcctgtgtgtgttcatttttacccctggcctgtcgtcgccgttcg 5455
 QY 80 ccgagcagtgccggctcgaagcggcgccggaagtcgcccactgctgtgtgtgcagcc 139
 Db 5456 ccgagcaatgcggaagcgaagccggggggtctctgccccggcggtgtgtgtgtagcc 5515
 QY 140 agttcgggttctgcggcaccacccctccgactactgcggcccccgtcgcagagccagtgc 199
 Db 5516 agtaagcgtgtgtgcggtatacagcaggtccatnctgcgtcaagatgccanaccatgcn 5575
 QY 200 ctggctgc-----ggtggcgggcgccgggggtggcctccatcgtgt 241
 Db 5576 cangctccacgcctcctccctccactcccgagcggtggcannngttgctcgatcata 5635
 QY 242 ccagggacotcttcgagcgttctcctccatcgcaacgacgagcgtcctgtgcccgcg 301
 Db 5636 tctctcctccttcnagcagatgctgaagcatcncanacgacnccgcccgcggaang 5695
 QY 302 ggtctacacgtacgacgctcttctggccgcggcgccgttcccggtccttcggcaca 361
 Db 5696 gcttctacnctnccgccttcctcctccgcgcgcacnctccttcancnggttcgggacna 5755
 QY 362 ccggagacctgcagacggcggaagcgggtgtggcgttcttcggccagacctctcag 421
 Db 5756 ccngcgaccctccacnaataanaungganatcncggttcttggtnacnctctcncg 5815
 QY 422 agaccacag----- 430
 Db 5816 agacnacangtaatcctnctnctcccgaggtcgtctcncagnttatnctatnctatnctn 5875
 QY 431 -----gcgggtggcccaacggccgcggccgcggcccttctcattggggc 471
 Db 5876 aatgcattgggttnggcacgtgggtgtccacgtgcccnaatgg-cnttcgctgggggt 5934
 QY 472 tactgttcaagcagcagcagcggcgcgcgcgactactgcgacccagagcgcgcactgg 531
 Db 5935 tactgttctccagnacagacccctcctcga-ctactgctgcgcagctcgcantgg 5993
 QY 532 ccgtgcgaccggcgaagcagtcactatgcccgcggcccccctccagctcaccacacactac 591
 Db 5994 ccgtgcgtgcangcaanaataactacgcccgaagcccccatacctcattcattcactac 6053
 QY 592 aactacgacccggcgccgcgcaatcgggggtggacctgtgtaacaaatccggacctgtg 651
 Db 6054 aactacggcgccggggaacacccatcgctccgacctgtcacaacccagacctgggtg 6113
 QY 652 gccacggcccgacagtggtgttcaagcggcgatattgttctggatgacgacgacgtcc 711
 Db 6114 gccacggcccgacacatctcctcgaagcgtctgtgtgttctgtgactcactcgtcg 6173
 QY 712 aacaagcctgtgcatgacgtgacgacggcggtgtgtgactccgacgcccaggggatagc 771
 Db 6174 cccaagcctgtgccaacgagtgataaccgggagctggagccatccaacgacggcg 6233
 QY 772 gcagccgacgggttaccgggtatgtgtcattcacaacacgtcattcacaacggggatccaa 831
 Db 6234 gcggccggaaggttccgggtcactcgtgttcacacacacatcattcattggaggtggag 6293
 QY 832 tgcgcgcatggcggaacgacaaaggtgcgactcggatcggtgttctcacaagcgtattgt 891
 Db 6294 tgcgggaaaggttcogactgcagggcggtggtatggacggcgttctcacaanaggtctgc 6353
 QY 892 gacatttctcgcatcgctacgggaataacctcgactgctacacacattgtcgttca 949
 Db 6354 gacttgcgtgggtgagctacggagacacttggactgctacacacattgtcgttca 6411

This is the nucleotide sequence of a DNA molecule termed ENDO. The invention provides isolated DNA molecules which are differentially expressed during banana fruit development, and the protein products of these genes. The DNA is selected from a group comprising starch synthase, chitinase, endochitinase, beta-1,3-glucanase, thaumatin-like protein, ascorbate peroxidase, metallothionein, lectin and senescence-related protein. The regulatory elements of the genes can be used to produce chimeric genes for transformation of plants to provide controlled expression of heterologous DNA during fruit development, or in response to exogenous developmental signals, such as ethylene signals. The heterologous protein, e.g. a therapeutic protein, can be isolated from the fruit or consumed directly in the transformed fruit. The identity of the present sequence is not given. The entire DNA sequence has been decoded in all 3 reading frames to provide the amino acid sequences given in AAY05842-44.

Sequence 7397 BP; 2109 A; 1549 C; 1592 G; 2012 T; 135 other;


```
XX 23-SEP-1997.
PD
XX
XX 19-APR-1993; 93US-0047413.
PF
XX
XX 29-JAN-1991; 91US-0647831.
PR
XX
XX (MOGE-) MOGEN INT NV.
PA
XX (UYLE-) RIJKSUNIV LEIDEN.
PA
XX
XX Bol JF, Cornelissen BJC, Linthorst HJM, Melchers LS;
PI Meulenhoff EJS, Sela-buurlage MB, Van ROEKEL JSC;
PI Vloemans AA, Woloshuk CP;
XX
XX WPI; 1997-479536/44.
DR
XX P-PSDB; AAB07513.
DR
XX
XX Fungus-resistant transgenic plants - containing genes encoding
PT intracellular chitinase and beta-1,3-glucanase
XX
XX Example 4; Fig 2; 42pp; English.
XX
XX This cDNA sequence encodes an intracellular chitinase which is used
CC to construct a transgenic plant in a novel method to produce plants
CC resistant to fungal attack. Such transgenic plants expressing an
CC intracellular plant chitinase gene and a plant beta-1,3-glucanase gene
CC within its tissues are predicted to exhibit improved resistance to
CC pathogenic fungi. Such genes should be operably linked to promoters and
CC terminators and optionally a gene encoding a selectable or screenable
CC trait. Plants that overexpress the chitinase and glucanase genes
CC exhibit a synergistic antifungal effect.
XX
XX Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;
SQ
```

```
Query Match 32.6%; Score 316.8; DB 18; Length 1152;
Best Local Similarity 61.5%; Pred. No. 8.1e-47;
Matches 545; Conservative 0; Mismatches 332; Indels 9; Gaps 2;
```

```
Db 548 ctggctcggaatatttcggacgagggcccatcccaatttcacacactacaactacggac 607
Qy 602 cggcgccgcgcgaatcgggtggagacctgtaacaatccggaacctgtggccacggacc 661
Db 608 ctgtgggaagcccataggagtgacctccctaaacaaacctgattgtggccacagatc 667
Qy 662 cgacagtgcgttcaagacgcgcatatgtctggtgacgacgagtcacaaacagccgt 721
Db 668 cagtaatctcattcaagtcagctctctggtttgttgactcctcaatcaccacaaacctt 727
Qy 722 cgtgcacatgacgtatcacgcggtgtgtggaacctccacagcgccagggatagcgacggac 781
Db 728 cttggcacgagtgcacatcattggaagatgcaacctcgtctgctgacggcgagccaatc 787
Qy 782 ggggtacccgggtatgtgtcatcaccaacgctcatcaacggcggtatccaatcgccatgg 841
Db 788 gtctccctggattgtgtcatcacgaacatcatcaatggtgcttgaatgtgtcgtg 847
Qy 842 ggcagaacgacaaggtggcggtatcggtgttctacaagcgctattgtgacatttcg 901
Db 848 gcaactgactcaaggtccaggatcgcatgtgggttttacaggagggtatgacgtatttcg 907
Qy 902 gcactggtacggggaataacctcgaactgctacacaaattgtcgtt 947
Db 908 gtgtagtctcgtgacaaattgttattggtggaaaccagaggtctt 953
RESULT 15
AAA58910
ID AAA58910 standard; cDNA; 1152 BP.
XX
AC AAA58910;
XX
DT 20-OCT-2000 (first entry)
XX
DE cDNA sequence encoding an extracellular chitinase.
XX
KW Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;
KW plant resistance; pathogenic fungi; fungal resistant plant; ss.
XX
OS Nicotiana sp.
XX
FH Key Location/Qualifiers
FT CDS 10..984
FT /tag= a
FT /product= "chitinase"
FT sig_peptide 10..78
FT /tag= b
XX
PN US6087560-A.
XX
PD 11-JUL-2000.
XX
PF 18-FEB-1997; 97US-0801563.
XX
PR 19-APR-1993; 93US-0047413.
PR 29-JAN-1991; 91US-0647831.
XX
XX (UYLE-) RIJKSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
XX
XX Cornelissen BJC, Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
PI Vloemans AA, Woloshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
XX
XX WPI; 2000-498214/44.
DR P-PSDE; AAB07513.
XX
XX New transgenic plants expressing chitinase and glucanase have improved
PT resistance against pathogenic fungi, particularly against Alternaria
PT alternata or Fusarium oxysporum f. sp. lycopersici -
XX
XX Example 4; Fig 2A-B; 42pp; English.
XX
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:26:33 ; Search time 142.45 seconds
(without alignments)
1545.361 Million cell updates/sec

Title: US-09-534-229C-7

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA.*
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6: /cgn2.6/prodata/2/ina/5B_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	496.6	51.1	1151	1	US-07-704-288C-2
2	496.6	51.1	1151	1	Sequence 2, Appli
3	496.6	51.1	1151	1	Sequence 1, Appli
4	469.4	48.3	1002	1	US-08-379-259-2
5	469.4	48.3	1002	1	Sequence 2, Appli
6	469.4	48.3	1002	1	US-08-457-797A-9
7	371.6	38.2	1225	1	Sequence 9, Appli
8	371.6	38.2	1225	1	Sequence 9, Appli
9	318.4	32.8	943	2	US-08-812-025-9
10	318.4	32.8	943	2	US-09-138-873A-9
11	316.8	32.6	1152	1	US-08-286-020-1
12	316.8	32.6	1152	1	US-08-603-919-1
13	316.8	32.6	1152	3	US-08-475-427-15
14	263.8	27.1	905	2	US-07-842-165-14
15	263.8	27.1	905	2	Sequence 15, Appli
16	196	20.2	1020	1	Sequence 15, Appli
17	196	20.2	1020	1	US-08-449-315-7
18	196	20.2	1020	1	Sequence 10, Appli
19	196	20.2	1020	1	US-08-444-803-7
20	196	20.2	1020	1	Sequence 7, Appli
21	196	20.2	1020	1	US-08-449-043-7
22	196	20.2	1020	1	Sequence 7, Appli
23	196	20.2	1020	1	US-08-456-265A-7
24	196	20.2	1020	1	Sequence 7, Appli
25	196	20.2	1020	2	US-08-455-244-7
26	196	20.2	1020	2	US-08-454-876-7
27	196	20.2	1020	2	Sequence 7, Appli
28	196	20.2	1020	2	US-08-457-364-7
29	196	20.2	1020	2	Sequence 7, Appli
30	196	20.2	1020	2	US-08-456-262-7
31	196	20.2	1020	2	Sequence 7, Appli
32	196	20.2	1020	2	US-08-456-240-7
33	196	20.2	1020	2	Sequence 7, Appli
34	196	20.2	1020	2	US-08-455-736-7
35	196	20.2	1020	2	Sequence 7, Appli

28	196	20.2	1020	2	US-08-971-217-7	Sequence 7, Appli
29	196	20.2	1020	4	US-09-350-600-7	Sequence 7, Appli
30	185.6	19.1	1317	3	US-07-791-931-1	Sequence 1, Appli
31	183	18.8	966	1	US-08-047-413-8	Sequence 8, Appli
32	183	18.8	966	3	US-08-229-050-8	Sequence 8, Appli
33	183	18.8	966	3	US-08-801-563-8	Sequence 8, Appli
34	175.2	18.0	968	1	US-08-181-271A-12	Sequence 12, Appli
35	175.2	18.0	968	1	US-08-449-315-12	Sequence 12, Appli
36	175.2	18.0	968	1	US-08-444-803-12	Sequence 12, Appli
37	175.2	18.0	968	1	US-08-449-043-12	Sequence 12, Appli
38	175.2	18.0	968	1	US-08-456-265A-12	Sequence 12, Appli
39	175.2	18.0	968	1	US-08-455-416-12	Sequence 12, Appli
40	175.2	18.0	968	1	US-08-455-244-12	Sequence 12, Appli
41	175.2	18.0	968	1	US-08-454-876-12	Sequence 12, Appli
42	175.2	18.0	968	2	US-08-457-364-12	Sequence 12, Appli
43	175.2	18.0	968	2	US-08-456-262-12	Sequence 12, Appli
44	175.2	18.0	968	2	US-08-456-240-12	Sequence 12, Appli
45	175.2	18.0	968	4	US-09-350-600-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-07-704-288C-2
; Sequence 2, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 51.1%; Score 496.6; DB 1; Length 1151;
Best Local Similarity 72.4%; Pred. No. 1.9e-98;
Matches 684; Conservative 0; Mismatches 234; Indels 27; Gaps 2;

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QY 834 cggcatggggcagacacaaagtgggcgatcgatcggtttacaaagcgtatttga 893
Db 897 CGGCATGGCGGAGGACGATCGATCGCGGACCGGATCGGCTTCTACAAAGGCTACTCGGA 956
QY 894 catttcggcatcggtacgggnaataacctcgactgtacaaacca 938
Db 957 CATCTCGGCTCAGCTACGCGGCCACTTGGATTGCTACAGCCA 1001

RESULT 4
US-08-457-797A-9
Sequence 9, Application US/08457797A
Patent No. 5689045
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic pathogen-resistant organism
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIP Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,797A
FILING DATE: June 1, 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..63
FEATURE:
NAME/KEY: CDS
LOCATION: 64..861
OTHER INFORMATION: /codon_start= 64
OTHER INFORMATION: /function= "chitinase"
OTHER INFORMATION: /product= "26 kD preprotein of chitinase G (ChiG)"
OTHER INFORMATION: /note= "antifungal activity, especially on
OTHER INFORMATION: Trichoderma reesei and Fusarium sporotrichoides as
OTHER INFORMATION: well as Rhizoctonia solani and Botrytis cinerea."
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 905..910

OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal peptide
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LOCATION: 349..378
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FEATURE:
NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
FEATURE:
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LOCATION: 607..861
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NAME/KEY: mat_peptide
LOCATION: 133..861
US-08-457-797A-9

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Best Local Similarity 76.6%; Pred. No. 3.5e-83;
Matches 575; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

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QY 258 ggggttcctgctccatcgaaacagcagcgtgcctggccggcggtttctacacgtacga 317
Db 168 CCGCATGCTTCTCCACCGCAACAGCAGCGCGCTTCCAGGCGCAAGGGCTTACACCTACGA 227
QY 318 cgcctttctggcgcgcgcgcgcttcccgcccttcggcaccacgcgagacctggacac 377
Db 228 CGCCTTCGTGCGCGCGCGCGCGCTTCCGGGCTTCGGCACCACCGGCGCGCGCGCAT 287
QY 378 gcggaagcgggaggtggcgcccttcttcggccagacctctcagagaccacggcggtg 437
Db 288 CCAGAAAGCGGAGGTGGCGCGCTTCTTAGCAGAGAGCTCCACGAGACCAACCGCGGGTG 347
QY 438 gccacacgccccgacggcccccttctcaggggtactcttcaagcaggagcagggtc 497
Db 348 GCGGACTGACCGGCGCGGCGCTTCCGCTGGGGCTACTGCTTCAAGCAGAGAGCTGGCGC 407
QY 498 ggcgcgagctactgcgaccagagcgccgactggcgccgaccccgcaagcagtaacta 557
Db 408 CTCCTCCGACTACTGTCACCCCGGAGCGCACAAATGGCGTGGCGCCCGGGAAGCGCTACTA 467
QY 558 tggcgcgcccccatccactcaccacccacataactacagcagcgggcgcgcaat 617
Db 468 CGGCGCGGCGGCAATCACTCTCCCACTTACAACTATGACCTGCGCGCGCGCGCAT 527
QY 618 csgggtggacctcgcaacaataccggacctgtggccacggaccgacagtggtgctaa 677
Db 528 CGGGGTGCGATCTGCTGGCGCAACCGGAGACTGCTGGCGACGCGGCGGCTTTAA 587
QY 678 gacggcgatgtgttctggtgacgacgcagtcacaaagcgtctgctgacgacgtaat 737
Db 588 GACGGCCATCTGGTCTGTGATGACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGTGAT 647

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Qy 738 cacgggggtgtgactcgcagcgccagggtatagcgcagccgggtacccgggtatgg 797
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Qy 798 tgcataccacagcgcacacggcggtatcaatgcggcatggcgagaaacagcaagt 857
Db 708 tctgataccacacacacacacacacacacacacacacacacacacacacacacac 767
Qy 858 ggcggatggatgggttctacacagcgctattgtgacatttctgcacatcggtacgggaa 917
Db 768 gcggatgcgaatcggttttacaagcgctactgtgacatcctcgccgttgctacggcaa 827
Qy 918 taactgcagctgtacacacacacacacacacacacacacacacacacacacacac 948
Db 828 caactcgatgtctacagccagacacacacacacacacacacacacacacacacacac 858

RESULT 5
US-08-812-025-9
; Sequence 9, Application US/0812025
; Patent No. 5804184
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,025
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tenser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Hordeum vulgare
; STRAIN: L.
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..63
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..861
; OTHER INFORMATION: /function= "chitinase"
; OTHER INFORMATION: /product= "26 kD preprotein of chitinase G (ChiG)"
; OTHER INFORMATION: /note= "antifungal activity, especially on
; OTHER INFORMATION: Trichoderma reesii and Fusarium sporotrichoides as
; OTHER INFORMATION: well as Rhizoctonia solani and Botrytis cinerea."
; FEATURE:
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; NAME/KEY: 3'UTR
; LOCATION: 862..1002
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 905..910
; OTHER INFORMATION: /note= "potential polyadenylation
; OTHER INFORMATION: signal"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 64..294
; OTHER INFORMATION: /note= "probable signal peptide
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 298..312
; OTHER INFORMATION: /note= "probable signal peptide
; OTHER INFORMATION: sequence"
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; NAME/KEY: sig_peptide
; LOCATION: 349..378
; OTHER INFORMATION: /note= "probable signal peptide
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 466..588
; OTHER INFORMATION: /note= "probable signal peptide
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 607..861
; OTHER INFORMATION: /note= "probable signal peptide
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..861
; US-08-812-025-9

Query Match 48.3%; Score 469.4; DB 1; Length 1002;
Best Local Similarity 76.6%; Pred. No. 3.5e-83;
Matches 575; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 198 cactggctgcgtggcgcggggtggccctccatcgtgtccagggaacctcttga 257
Db 108 CATGCCCATCGCACGGCGCGCGGCGCTCTCTCCATCGTCTCGCGCACAGTTTGA 167
Qy 258 gcggttctctgctccatcgcaacgacgacgagtgctggcccgcggtttctacagta 317
Db 168 CCGCATGCTTCTCCACCGCAACGACGGCGCTGCCAGGCCAAGGCGCTTCTACCTACGA 227
Qy 318 cgccttctggcgccgcggcggttcccgcccttcggccaccgagagacctggacac 377
Db 228 CGCCTTGTGTCGGCGCGCAGCGCGCTTCCGGGCTTGGCACCCACCGCGCGGCGGC 287
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Db 288 CCAGAAGCGCGAGGTGGCGCGCTTCTCTAGCACAGACCTCCACGAGACACACCGCGGGTG 347
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Db 348 GCGGACTGCACCGGACGGGGCGCTTCGCCCTGGGGTACTGTCTCAAGCAGGAACGTGGCGC 407
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Qy 558 tggcgggggccccctccagctcaaccacacataactacgagcggcgggcgccgcaat 617
Db 468 CGGCGCGGGCGCAATCCAGCTCTCCCAACAACATACAACTATGGAATGCTGCGCGCGGCAT 527
Qy 618 cggggtggacctgctgaacaataatccggacctggtggccacggacacagtgcggttaa 677
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Db 408 CTCCTCGACTACTGACCCCGAGCGGCACAAATGGCGCGCCCGGGAAGCGCTACTA 467
QY 558 tggccgcccacatccagctcacccacaactacaactagcagccgcccgcgcgcaat 617
Db 468 CGGCGCGGGCCCAATCCAGCTCTCCCAACAACACTATGAGACTCCCGCGGGCCAT 527
QY 618 cggggtgagactgctgaacaatccggacctgggtggccacggaccgacagctgggttcaa 677
Db 528 CGGGGTGATGCTGTGTCGCAACCGGACCTGGTGGCCACGACGCCCACTGTGGCTTTAA 587
QY 678 gagggcgatggtctggtgtagcagcagcagtcacaaagccgctgctgacatgacgtgat 737
Db 588 GACGCCCATCTGTTCTGGATGACGGCGGACCGCCGCCCAAGCCATCGAGCCCATGTGTGAT 647
QY 738 caagggtgtagactcgacgagccagggtagcagcagcggagcgggtaccccggtatgg 797
Db 648 CGCGGCGCAGTGGAGCCGCTCAGGGGTGACCGGGCGCGCAGCGCGGTGCCCGGGTTGG 707
QY 798 tgtcatcacaacgctcaatacagggcgagtcacatgagcagcatggggcagacagcaaggt 857
Db 708 TGTGATCACCACAATCATCAACGGCGGGATCGAGTGGCGTACGGCGGACGACAGCCGCGT 767
QY 858 ggcggtcgatcggtgtctacaagcgtattgtgacattttcgccatcggctacgggaa 917
Db 768 CGCGATCGAATCGGTTTACAGCGCTACTGACATCTCTCGGCGTTGGCTACGGCAA 827
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Db 828 CAACCTCGATTGTACAGCGCAGACCCCTTC 858

RESULT 7
US-08-286-020-1
; Sequence 1, Application US/08286020
; Patent No. 5539095
; GENERAL INFORMATION:
; APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
; TITLE OF INVENTION: A Chitinase cDNA Clone from a
; TITLE OF INVENTION: Disease Resistant American
; TITLE OF INVENTION: Elm Tree
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS 5.00
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,020
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5539095e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1225
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
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; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Ulmus Americana
; STRAIN: NPS 3-487
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE: N/A
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: chitinase encoding DNA
; LOCATION:
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: DNA needed for chitinase
; OTHER INFORMATION: in elm.
; PUBLICATION INFORMATION:
; US-08-286-020-1
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Query Match 38.2%; Score 371.6; DB 1; Length 1225;
Best Local Similarity 64.5%; Pred. No. 3.3e-64;
Matches 573; Conservative 0; Mismatches 309; Indels 6; Gaps 1;

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QY 193 cagtgcactgctgcgtggcgcgcgcggggtgacctccatcctgctgcagggacctc 252
Db 262 CAATGTGGCGCAGCGGTAGCGATGAC-----ATTGGGGTCTCATATCAAGTCCGCC 315
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Db 376 TATGATGCTTTTATTGCGGTGCGCAAGGCTTTCCCTGCATTTGGCTCCACCGGGGATGAT 435
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Db 436 ACCACCGTAAAGGGAGATTGCTGCTTTCTTAGGTCAAACTTCCCATGAACACTACAGGT 495
QY 433 ggttgcccacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 492
Db 496 GGGTGGGCAAGTGCACCCGACGGTCCATACTCTTTGGGATCTGCTACTAATAGGGAGCAA 555
QY 493 ggtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 552
Db 556 AACCTTCTCCGATTATTGTTCTTTAGTCTTACTTGGGCTTGTGCTTCGGAAAGAGA 615
QY 553 tactatgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 612
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QY 613 gcaatcggttgacctgctgaacaatcccgacctggtggccacggaccgcagctggcg 672
Db 676 GCCATAGGCAAAACCTATTAAACAACCCCTGATCTCGTAGCAACTGACCTGTCAATTC 735
QY 673 ttaagacgcgatatggttctgtagatgacgcagctccaaagccgctgctgacctgac 732
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPFAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 905 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-842-165-14

Query Match 27.1%; Score 263.8; DB 2; Length 905;
Best Local Similarity 59.9%; Pred. No. 2.6e-43;
Matches 505; Conservative 0; Mismatches 317; Indels 21; Gaps 3;

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QY 71 cggccacgagcagtcggtcgcaagccgagcgcgcaagtcgacgactgacgactgctgt 130
Db 62 CTGCTGGCACAGAAATGGTTCACAGCGCGGAGGCAAGTTTGCGTCGGGACAAT 121

QY 131 gctgcagcagttcgggttcctgcggcaccacctccgactactcgccccgc---tgcc 187
Db 122 GTTGACAGAAATCGGTGTCGGGTAACTAATGACCATTTGGTTCTGGCAATTGTC 181

QY 188 agagcaagtgcactgctggtggtgggc-----ggcgaggggtggcct 232
Db 182 AAGTCAGTGTCCAGGTGGCGGCGCTGCTGCTGCTGTTACTGTTGGTGGGACCTCGAA 241

QY 233 ccactggttcagggacctcttcgagcggttcctgcctccatcgcaacgacgacgctgccc 292
Db 242 GCGTCATCTCAATTCATGTTTGATCAATGCTTAGCAATCGTAACGAAAATTCCTGTC 301

QY 293 tgg---cccggggttacacgtacgacgactcttggccgcgcgcggcggttcocgg 349
Db 302 AAGGAAAGAAATAATTTACAGTTACAGTTCATGCTTAATGCTGCTGCTAGGTCCTTCCTG 361

QY 350 ctttcgacacacgagacactggacacgagggagggaggggtggcgaccttcttcggcc 409
Db 362 GCTTTGTACAAGTGGTGATATCAATGCCGTAAAGGGAATGCTGCTTCCTTCCTGCC 421

QY 410 agacctctcagagaccacggcggtggccccaccgccccgcgccccctctctcagg 469
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Search completed: May 3, 2002, 16:27:02
Job time: 7296 sec

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Db 422 AAACCTCCCATGAAACTACTGGAGATGGCTTCCGCACTGATGGACCATTCGCATGGG 481
QY 470 gctactgcttcaagcaggagcagggctcgccgcgagctactcgaccacgagcgcgact 529
Db 482 GTTACTGTTTCCCTTAGAGAAACGAGGTAAOCCCGGTGACTACTGTTCCACCAAGTAGTCAAT 541
QY 530 ggccgtgcgaccccgcaacgacgactactatggccgcgccccccatccagctcaccacaaact 589
Db 542 GGCTTTGTGCACCTGGAAGGAATATTTCCGACGAGGCCCAATCCAAATTTACACAACT 601
QY 590 acaactacggaccggcgccgcgcgaatggggtgacotgctgaaacatcccggaactgg 649
Db 602 ACAACTATGGCCCATGTGGAAGAGCCATCGAGTGGACCTTTTAAACAATCTGATTAG 661
QY 650 tggccacgacccgacacagtggttcaagacgagcgatattggttctggtgatgacgacgact 709
Db 662 TAGCCACAGACCCAGTCATCTCAAGACTGCTATCTGGTCTGGATGACCCCTCAAT 721
QY 710 ccaacaagccgtcgtgcatgacgtgacggggtggtgactccgacgagcgagggata 769
Db 722 CACCAAGCCCTTCTTGCCACGATGTCATCATTTGAAGATGGAACCCCATCTGCCGTGACC 781
QY 770 ggcgagccgacgggttacccgggtatggtgtcatccacacgctcatcaacgagcgatcc 829
Db 782 GATCAGCCAAATCGTCTCTCTGATTTGGTGTCTATCAAAACATCATCAATGGGGGCTGG 841
QY 830 aatgcgcatggcgagacgacgacgaggtgcgagatcggttcggttctacaagcgtatt 889
Db 842 AATGTGTCGTGGCAATGACAAATAGGGTCCAAAGATCGCATTTGGGTTTTACAGAGGTATT 901
QY 890 gtg 892
Db 902 GCG 904
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:23:53 ; Search time 3076.35 seconds
(without alignments)
3395.224 Million cell updates/sec

US-09-534-229c-7

Title:

Perfect score:

Sequence:

1 agtcaocagctgagagcgcg.....ttgggctcgcgacagtgta 972

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estfun:*

2: em_esthum:*

3: em_estin:*

4: em_estom:*

5: em_estpl:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_est1:*

11: gb_est2:*

12: gb_hic:*

13: gb_gss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_inv:*

17: em_gss_pln:*

18: em_gss_pro:*

19: em_gss_rod:*

20: em_gss_vrt:*

21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	685.4	70.5	816	11 BF064981	HV_CEB002
2	566.4	58.3	652	10 AL499683	AL499683
3	533.6	54.9	693	10 AL500402	AL500402
4	520.2	53.5	616	10 BE405578	BE405578
5	471.6	48.5	508	10 BE430003	TAS006.A0
6	466.2	48.0	480	11 BG263207	WHE2339_C
7	455.6	46.9	805	11 BG365536	HVSMEL000
8	454.2	46.1	584	10 BE455567	BE455567
9	429	44.1	935	11 BG365857	HVSMEL000
10	422.4	43.5	617	11 BF619746	HVSMEL000
11	414.2	42.6	729	10 BE602672	BE602672
12	413.8	42.6	482	10 BE488961	WHE1077_C

13	403.8	41.5	623	11	BG368852	BG368852
14	403.6	41.5	937	11	BG365887	BG365887
15	403	41.5	498	10	BE425245	WHE313_A0
16	396.6	40.8	742	11	BG365634	BG365634
17	396	40.7	653	11	BG313150	WHE2054_D
18	394.4	40.6	682	11	BG416746	BG416746
19	394.4	40.6	806	11	BG414551	BG414551
20	392.4	40.4	402	10	BE498719	WHE0965_F
21	389.6	40.1	485	11	BF624146	HVSMEL002
22	389.2	40.0	625	11	BG368854	BG368854
23	385.2	39.6	681	10	BE705117	Sc02_08b0
24	377.6	38.8	908	11	BG415203	HVSMEL000
25	372.4	38.3	731	10	BE602548	BE602548
26	370.8	38.1	969	10	BE454366	HVSMEL009
27	363.4	37.4	711	11	BG366386	BG366386
28	356.4	36.7	711	10	BE455238	HVSMEL009
29	355.2	36.5	899	10	BE603335	BE603335
30	354	36.4	489	10	BE411224	ISC003.D0
31	350.8	36.1	692	11	BG369588	BG369588
32	350.8	36.1	705	11	BG367460	HVSMEL001
33	350.6	36.1	753	11	BG365326	BG365326
34	346.4	35.6	432	11	BF620099	HVSMEL000
35	346	35.6	717	10	BE454845	BE454845
36	345.4	35.5	613	10	BE425368	WHE313_F0
37	345.2	35.5	943	11	BG365157	BG365157
38	342	35.2	487	10	BE426069	WHE0327_A
39	340.4	35.0	711	11	BG367616	HVSMEL001
40	339.4	34.9	912	11	BG301220	HVSMEL001
41	338.2	34.8	710	11	BG366294	BG366294
42	338	34.8	503	11	BG907369	TALr1159E
43	333.6	34.3	652	10	BE602137	HVSMEL010
44	328.2	33.8	632	10	BE598085	BE598085
45	327.8	33.7	333	10	BE405888	WHE0401_d

ALIGNMENTS

RESULT 1
BF064981
LOCUS
HV_CEB0022E17f Hordeum vulgare seedling green leaf EST library
DEFINITION
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEB0022E17f, mRNA sequence.
ACCESSION
BF064981
VERSION
BF064981.2 GI:13266369
KEYWORDS
EST.
SOURCE
barley.
ORGANISM
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 816)
Wing, R., Close, T.J., Klein, R., Wise, R., Begum, D., Frisch, D., Yu
Y., Anderson, H., Dale, J., Henry, D., Kern, S., Palmer, M., Rambo
T., Saski, C., Schwartz, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
JOURNAL
On Oct 17, 2000 this sequence version replaced gi:10841620.
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCCTACTAAAGG
High quality sequence stop: 792.
FEATURES
Location/Qualifiers
1..816
/organism="Hordeum vulgare"

Query Match 54.9%; Score 533.6; DB 10; Length 693;
Best Local Similarity 91.6%; Pred. No. 1.4e-88;
Matches 597; Conservative 0; Mismatches 51; Indels 4; Caps 3;

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quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
FEATURES
    source
        1..616
            /organism="Triticum aestivum"
            /cultivar="Chinese Spring"
            /db_xref="taxon:4565"
            /clone="WHE1209_A02_A03"
            /clone_lib="Wheat etiolated seedling root cDNA library"
            /tissue_type="Root"
            /dev_stage="Five day old etiolated seedling"
            /lab_host="E. coli SOLR"
            /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                Site1: EcoRI; Site2: XhoI; Seeds were surface-sterilized
                , germinated and grown aseptically in the dark at room
                temperature on filter paper with water, nystatin and
                cefotaxime in covered crystallization dishes. Roots were
                harvested. The tissue, total RNA, and poly(A) RNA clones
                prepared. A cDNA library was made, and the cDNA clones
                were in vivo excised to give pBluescript phagemids in the
                TJ Clouse lab (Choi, Clouse, Fenton) at the University of
                California, Riverside. Plasmid DNA preparations and DNA
                sequencing were performed in the OD Anderson lab (all
                other authors)."
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BASE COUNT 110 a 211 c 190 g 105 t

ORIGIN

Query Match 53.5%; Score 520.2; DB 10; Length 616;
 Best Local Similarity 91.2%; Pred. No. 4e-86;
 Matches 563; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Qy 120 cgactgtgtgtgcagccagttcgggtttctggcggcaccacctccgactactcggccc 179
 Db 1 CAACGTGCTCTGTCGACGCAATTCGGGTTCTGCGGACGACCTCCGACTACTCGGTTG 60

Qy 180 ccgctgcccagagccagtgactgctgcgtggcgggcggggtggcctccatcgt 239
 Db 61 CGGTGCCAGAGCCAGTGCATGCTGCGGGCGGACGAGCGCGGTGGGTGTGCATCATCGT 120

Qy 240 gtcagggaacotcttcgagcgttctctctcctcgcacgacgacgagcgtgcctggccg 299
 Db 121 TTCAGGGAGCCTCTTCGATCGTTCTCTCTCATCGCAACGACGCGCGTGCCTGGCCG 180

Qy 300 cgggtttacacgtacacgacctcttgcgcgcgcgcgcgcgttcccggtcttcggcac 359
 Db 181 CGGTTCTACACCTACGACGCGCTTCTTGCCGCCGCCAGCGGTTCCGCGCTTCTGCAC 240

Qy 360 caccggagacctggacacgcggaagcggagtggtggcgcttcttcggccagacctca 419
 Db 241 CACGGGAGACTTGGACACGCGGAACGAGAGGTGCGGCTTCTTCGCGCCAGACCTCTCA 300

Qy 420 cgagaccacggcggtggccacacgcgcgcgcgcgcgcgcgttcttcggtggtactgttt 479
 Db 301 CGAGACCAACCGCGGTGGGCGCCACGCGACCGCGGCGCTTCTCATGGGGTACTGCTT 360

Qy 480 caagcagagcaggtgc 539
 Db 361 CAAGCAGGAGAGATCCGCGGGAAGTACTTGCAGCAGCAGCGCGCTGCGCGCGCG 420

Qy 540 acccggaagcagtgactatggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 599
 Db 421 GCCCGGAAGCAGTACTACGGCGCGGCGCCCATTCAGCTCACTCACTCACTCACTATGG 480

Qy 600 accgcgggcgccgaatcgggtggacgtcgtgacacatccggacctgtggccacgga 559
 Db 481 ACCGTGGGCGCGCAATCGGGGTGACCTGTGTAAACAACCGGACCTGTGTGCGC-CGGA 539

Qy 660 cccgacgtggcgttcaagacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 719
 Db 540 CCCGACGGTGGCGTTCAGACAGCGCCATCTGGTCTGGATGACGACGACGACGACGAC 599

Qy 720 gtcgtgcatgacgtga 736

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Db 600 GTCATGCCATGACGTGA 616

RESULT 5
BE430003
LOCUS BE430003 508 bp mRNA EST 26-JUL-2000
DEFINITION TAS006.A08R990616 ITEC TAS Wheat cDNA Library Triticum aestivum
cDNA clone TAS006.A08, mRNA sequence.
ACCESSION BE430003
VERSION BE430003.1 GI:9427846
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE 1 (bases 1 to 508)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorrells,M., Warburton,M. and Wenzel,G.
International Triticaceae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticaceae
JOURNAL Unpublished (2000)
COMMENT Contact: Selvaraj G
Plant Biotechnology Institute, National Research Council of Canada
110 Gymnasium Place, Saskatoon, SK S7N 0W9 Canada
Tel: 306 975 5577
Fax: 306 975 4839
Email: Gopalan.Selvaraj@nrc.ca
International Triticaceae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES
    source
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            /db_xref="taxon:4565"
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            /clone_lib="ITEC TAS Wheat cDNA Library"
BASE COUNT 66 a 188 c 175 g 79 t
ORIGIN

Query Match 48.5%; Score 471.6; DB 10; Length 508;
Best Local Similarity 97.8%; Pred. No. 3.2e-77;
Matches 499; Conservative 0; Mismatches 9; Indels 2; Gaps 2;


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    Db 1 CAGGCTGAGAGCGCGGTGTGCGACGCGCTCTGCGCGCTCTGCTGCGCGCGCGCGCGGT 60



Qy 66 cagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 125  

    Db 61 CAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120



Qy 126 cctgtgctgcagcagcttcggttctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 185  

    Db 121 CTTGTGCTGCAGCCAGTTCGGGTTCGTGCGGACACACCTCCGACTCTGCGCGCGCG 180



Qy 186 ccagagccagtgcaactgctgctgctgctgctgctgctgctgctgctgctgctgctgct 245  

    Db 181 CCAGAGCCAGTGCATGCTGCTGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240



Qy 246 ggacaccttcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 305  

    Db 241 GGACCTCTTCGAGCGGTTCCTGCTCATCGCAACACGACGCGCTGCGCGCGCGCGGT 300



Qy 306 ctacacgtacgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 365  

    Db 301 CTACACGTACGACGCGCTTCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360


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QY 366 agacctgacacgagcgagggtggcgcccttcttctggccagacctctcacagac 425
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Db 361 AGACTGGACACGGGAGCGGAGGTGGCGGCTTCTTGCGCCAGACCTCTCAGGAGAC 420
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QY 426 caccggcggtggccaccgcccagcgcccttctctatcctggtggtactcttcaagca 485
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Db 421 CACCGGGGGTGG-CCACCGGGCGCCGACGCCCTTCT-ATGGGGTACTGCTTCAACA 478
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QY 486 ggaacaggtcgccgcgagctactcgca 515
|||||
Db 479 AGACGAGCTGGCGCGAAGTACTACGCA 508
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RESULT 6
LOCUS BG263207 480 bp mRNA EST 16-FEB-2001
DEFINITION WHE2339_c11_F21ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2339_c11_F21, mRNA sequence.
ACCESSION BG263207
VERSION BG263207.1 GI:12865133
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 480)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.B. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1..480
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2339_c11_F21"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid:
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
83 a 174 c 151 g 71 t 1 others

BASE COUNT 83 a 174 c 151 g 71 t
ORIGIN

Query Match 48.0%; Score 466.2; DB 11; Length 480;
Best Local Similarity 98.1%; Pred. No. 3.1e-76;
Matches 471; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 260 ggttctgtctatcgcacgacgagctgctgctgcccgcgggttctacacgtacgacg 319
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Db 1 GGTCTCTCTCCATCGCAACGACGCGCGGTGCCTGGCCCGCGGGGTCTTACACGTACGACG 60
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QY 320 ccttttggccgcgcgcgcgcgttccccggccttcggccaccacggagaccttgacacgc 379
|||||
Db 61 CTTTCTTGGCGCGCGCGCGGTTCGCGCTTCGGCCACACCGGAGACCTGGACACGC 120
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QY 380 ggaagcgggagtggtggcgccttcttctggccagacctctcacgacacacacggcggtggc 439
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Db 121 GGAAGCGGGAGTGGCGCGCTTCTTTCGGCCAGAGCTCTTCAGGAGACCAACCGCGGGTGGC 180
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QY 440 ccacggcgccgcgacgccccttctctatggtggtactgttcaagcagagcagggctcgc 499
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Db 181 CCACCGCGCGCGCGCGCTCTCTATGGGGTACTGCTTCAAGCAGAGAGCGGGCTCGC 240
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QY 500 cgcgagctactggacacagcgccgactggcgcctggcgcacccggcgaagcagtactatg 559
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Db 241 CACCGAGCTACTGCGAOCAGAGCGCGCTGCGCTGCGCACCCGCAAGCAGTACTATG 300
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QY 560 gccggggcccatccagctcaccacaactacaactacgacggcgccggcgccgcaatcg 619
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Db 301 GCCGCGCGCGCGCGCTCAGCTCAGCCCAACTACACTAGGACCAACGCGCGCTGGGATCG 360
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QY 620 ggttgacctgctgaacaatccggacctgtggccacgacccgacagtggcggttcaaga 679
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Db 361 GGGTGACCTGCTGACAACTCGGACCTGGTGGCCACGACCCGACGGTGGCGTTCAAGA 420
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QY 680 cggcatatggttctgtagcagcagcagtcacaaagccgctgctgacctgacgtatgac 739
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Db 421 CCGGATATGTTCTGGATGACGACGAGTCCACAAGCGCTCGTGCATGACGTGATCA 480
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RESULT 7
LOCUS BG365536 805 bp mRNA EST 08-MAR-2001
DEFINITION HVSM010003B22f Hordeum vulgare 20 DAP spike EST library HVCN0010
(20 DAP) Hordeum vulgare cDNA clone HVSM010003B22f, mRNA sequence.
ACCESSION BG365536
VERSION BG365536.1 GI:13254635
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 805)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 778.
Location/Qualifiers
1..805
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSM01003B22f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HVCN0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
source

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Qy 579 caccacaa 587
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Db 489 CACTCACAA 497

Search completed: May 3, 2002, 16:24:10
Job time: 7210 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 15:36:53 ; Search time 3990.51 Seconds
(without alignments)
3968.739 Million cell updates/sec

Title: US-09-534-229c-8

Perfect score: 960

Sequence: 1 atgagaggagtgtgtgtgtgt.....accaaagccgttcgcatag 960

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_om:**

20: em_or:**

21: em_ov:**

22: em_pat:**

23: em_ph:**

24: em_pl:**

25: em_ro:**

26: em_sts:**

27: em_sy:**

28: em_un:**

29: em_vi:**

30: em_htgo_hum:**

31: em_htgo_inv:**

32: em_htgo_rod:**

33: em_htg_hum:**

34: em_htg_inv:**

35: em_htg_rod:**

36: em_htg_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	875	91.1	1985	8	TACHIG	X76041 T.aestivum
2	852.8	88.8	1192	8	AF280437	AF280437 Secale ce
3	800.4	83.4	1173	8	AF000965	AF000965 Poa prate
4	796.6	83.0	1080	8	AF000966	AF000966 Poa prate
5	777.4	81.0	1252	8	AF000964	AF000964 Poa prate
6	634	66.0	2808	8	RICCHT3	D16223 Rice Cht-3
7	634	66.0	141534	2	AP003685	AP003685 Oryza sat
8	630.8	65.7	1684	8	HVU02287	U02287 Hordeum vul
9	629.6	65.6	1191	8	AB051578	AB051578 Secale ce
10	621	64.7	2739	8	RICCHT1	D16221 Rice Cht-1
11	614.6	64.0	1151	6	I84465	I84465 Sequence 2
12	612	63.8	1160	8	OSEUDO	X56063 O.sativa mr
13	598.4	62.3	1186	8	OSLMNAC	X56787 O.sativa L.
14	589.2	61.4	1237	8	OSCHIT	X54367 Oryza sativ
15	577.6	60.2	2048	8	OSDNARC24	X87109 O.sativa RC
16	574.8	59.9	1159	8	OSCHITIA	Z29961 O.sativa (P
17	573.6	59.8	1291	8	RICCHITA	L37289 Oryza sativ
18	557.4	58.1	1779	8	BLYCHI33A	L34211 Hordeum vul
19	530.8	55.3	1051	8	OSU0286	U02286 Oryza sativ
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21	513.6	53.5	998	8	BLYCHI	M62904 H.vulgare L
22	513.6	53.5	1002	6	A37990	A37990 Sequence 9
23	513.6	53.5	1002	6	AR037574	AR037574 Sequence
24	513.6	53.5	1002	6	I75200	I75200 Sequence 9
25	513.6	53.5	3169	8	BLYCHI26A	L34210 Hordeum vul
26	491.8	51.2	1128	8	MZECHITC	L00973 Zea mays ac
27	470.8	49.0	1100	8	OSCHITIB	Z29962 O.sativa (P
28	458.4	47.8	2986	8	RICCHT2	D16222 Rice Cht-2
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30	439.8	45.8	1280	8	AB018248	AB018248 Oryza sat
31	428.4	44.6	1120	8	PACHI1	Z78202 Persea amer
32	408.8	42.6	1012	8	MZECHITINA	L16798 Zea mays cl
33	400	41.7	1085	8	ALCCHITINA	M94105 Allium sati
34	392	40.8	556	8	HVENDCHT	X15349 Barley (H.v
35	387.2	40.3	1132	8	PHVCHM	M13968 P.vulgaris
36	377.2	39.3	1058	8	AB015655	AB015655 Cucurbita
37	376	39.2	4704	8	S43926	S43926 CH5B-chitin
38	375.4	39.1	1132	8	NTECHITR	X16939 Nicotiana t
39	371.8	38.7	1070	8	AB048531	AB048531 Psophocar
40	371.6	38.7	1007	8	ALCCHINTIA	M94106 Allium sati
41	369.2	38.5	879	6	E13289	E13289 cDNA encodi
42	369.2	38.5	998	6	E13290	E13290 cDNA encodi
43	365.4	38.1	1670	8	PEACHI2I	L37876 Pisum sativ
44	362.6	37.8	1156	8	S44869	S44869 basic chiti
45	359.8	37.5	892	8	AF307511	AF307511 Vigna ses

ALIGNMENTS

RESULT 1

TACHIG	TACHIG	1985 bp	DNA	PLN	02-AUG-1996
LOCUS	T.aestivum (Chinese spring)	chi gene for endochitinase.			
DEFINITION	X76041				
ACCESSION	X76041.1	GI:416028			
VERSION	CHI gene; endochitinase.				
KEYWORDS	bread wheat.				
SOURCE	Triticum aestivum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticeae; Triticum.				
REFERENCE	1 (bases 1 to 1985)				
AUTHORS	Liao,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH, Worringer Weg, 52056 Aachen, FRG				
REFERENCE	2 (bases 1 to 1985)				
AUTHORS	Liao,Y.C., Kreuzaler,F., Fischer,R., Reisener,H.J. and Tiburzy,R.				
TITLE	Characterization of a wheat class Ib chitinase gene differentially				

Db	766	AAACCTTCGAGCCACGACGTATACGGGCGGTGGAGCCCTCGGGCGCCGACACGACA	825
QY	781	gcggggagggtgcctggggtacggtgtgatcaccacaatcatcaacggtgggtcgatgctgc	840
Db	826	CGGGTAGGTTGCTGGGTACGGGTGATCACCACATCATCACGGTGGGTCTGAGTGC	885
QY	841	gggcgggcaggacgcccgtgtccgcacgcatcggtttctacaacgctactctgcac	900
Db	886	GGGCGGGGAGGATGCTGCTGTCGCCACCGAATCGGGTTCATCAACGGTACTGTGAC	945
QY	901	ctccttgcgtcagctacggtgacaaactgactgtctacaaacaaagcccttgcacatg	960
Db	946	CTCTCGGGTCACTACGGGCCACAATCTGGACTGCTACAAACGAGGCCGTGCGCATAG	1005
RESULT 3			
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LOCUS	AF000965	1173 bp	DNA PLN 31-OCT-1999
DEFINITION	Poa pratensis chitinase (Chi3) pseudogene sequence.		
ACCESSION	AF000965		
VERSION	AF000965.1 GI:6164586		
KEYWORDS	kentucky bluegrass.		
SOURCE	Poa pratensis		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poaceae; Poa.		
REFERENCE	1. (bases 1 to 1173)		
AUTHORS	Du, M. and Ha, S.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley, CA 94706, USA		
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CDS	194..346		
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QY	61	gagcaatcggtctcagcgccggggcgacgtgccccaactgcctctgctgcagcaag	120
Db	254	GAGCAGTGGGCTCGCAGACGAGCGGGGGAGCTGCCCAACTGCTGCTGCGACAAAG	313
QY	121	ttcggtttctgcgcacacacctccgactactcggcacccggtgccagagccagtgcatt	180
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QY	181	ggctgcagggcgccaccccggtatccggtaccgcaccccttcggggggggtctctctcc	240
Db	374	GGCTGGGGGGTCCACGCGGTT---GACCCCGACTCCCTCCGGGGGGCGGTGTCCTCC	430
QY	241	attatctcgagctcctcttcgacacagatgctgtgcaccgcaacgacgagcggtgcctg	300
Db	431	ATCATATCCCACTGCTCTCTGAACAGATGCTTCTGACCGCAACGACGCGCGTGCCTG	490
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QY  166  cagagcgaagtcaatggctgcagggcgccgaccccggtaccgggtaccgacacccctccggc 225
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Db  19894  CAGAGCCAGTGTCTGGCGGCTGCGGCGGCGGCGCCGACCCGCGCTCCAGCGTGGCGGC 19835

QY  226  ggcggcgctctctccattatctcgagtcgctcttctcgaccagatgctgctgcacgcgaac 285
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Db  19834  AGCGCGTCTCATATCATATCGCCCTCGCTCTTCGACCCAGATCTGCTCCACCGCAAC 19775

QY  286  gacggcggtcctgcgcgaaggggtttacaactacggcgcccttgctgcgcgcgaac 345
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Db  19774  GACCAAGCGGTGCGCGCTTAAGGGCTTCTACACTACGACGCGCTTGTGCGCGCGCCCAAC 19715

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QY  406  ttctctctcagaactccacagagacgacggcggttggtggcgacggcgcccgacggcccc 465
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RESULT 9
AB051578
LOCUS Secale_cereale rsca mRNA for seed chitinase-a, complete cds. 25-NOV-2000
DEFINITION Secale_cereale rsca mRNA for seed chitinase-a, complete cds.
VERSION AB051578
KEYWORDS AB051578.1 GI:11344586
SOURCE Secale cereale cDNA to mRNA.
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Secale.
REFERENCE
1 (sites)
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AUTHORS Ohnuma,T., Yamagami,T. and Ishiguro,M.
TITLE Cloning and Sequencing of the Rye Seed Chitinase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1191)
AUTHORS Ohnuma,T., Yamagami,T. and Ishiguro,M.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-2000) to the DDBJ/EMBL/GenBank databases. Takeshi Yamagami, Kyushu University, Protein Chemistry and Engineering, Faculty of Agriculture; Hakozaki, 6-10-1, Fukuoka, Higashi-ku, Fukuoka 812-8581, Japan (E-mail:yamagami@uclink.berkeley.edu, Tel:81-92-642-4218, Fax:81-92-642-3051)

FEATURES
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Db 1015 TTGCTTA 1022

RESULT 10
LOCUS RICCHT1
DEFINITION Rice Cht-1 gene for endochitinase, complete cds.
ACCESSION D16221
VERSION D16221.1 GI:452232
KEYWORDS endochitinase.
SOURCE Oryza sativa (sub_species japonica, strain Nipponbare) DNA, clone
RG31.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 2739)
AUTHORS Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
TITLE Sequence variation, differential expression and chromosomal
location of rice chitinase genes
JOURNAL Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
MEDLINE 94049667
REFERENCE 2 (bases 1 to 2739)
AUTHORS Nishizawa,Y.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko
Nishizawa, National Institute of Agrobiological Resources, Rice
Genome Research Program; 2-1-2 Kannondai, Tsukuba, Ibaraki 305,
Japan (E-mail:CS.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
COMMENT Submitted (11-MAY-1993) to DDBJ by:
Yoko Nishizawa
National Institute of Agrobiological Resources
2-1-2 kannondai
Tsukuba, Ibaraki 305
Japan
Phone: 0298-38-7451
Fax: 0298-38-7408.
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:32:50 ; Search time 309.71 Seconds
(without alignments)
2657.429 Million cell updates/sec

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Scoring table: IDENTITY NUC
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Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854.6	89.0	954	AA24889	Rye chitinase-like
2	614.6	64.0	1151	AAQ31408	RC10 chitinase ge
3	614.6	64.0	1151	AAQ81346	Rice chitinase RCH
4	611.4	63.7	3035	AAF54983	Nucleotide sequenc
5	600.2	62.5	1163	AA96224	cDNA encoding a ma
6	513.6	53.5	1002	AAQ62518	Sequence encoding
7	441.4	46.0	1318	AAV49982	Floral organ-speci
8	379.2	39.5	7397	AA25613	Banana ripening fr
9	374.4	39.0	4704	AAQ05264	Sequence encoding
10	369.2	38.5	879	AAT79940	Chitinase coding s
11	369.2	38.5	998	AAT79941	Full length chitin

12	358	37.3	1225	17	AAT33325	American elm chiti
13	347.6	36.2	1152	12	AAQ12898	Tobacco intracellu
14	347.6	36.2	1152	18	AAT89952	Nicotiana sp. intr
15	347.6	36.2	1152	21	AAA58910	cDNA sequence enco
16	323	33.6	721	20	AAV59461	Banana fruit ripen
17	320.8	33.4	755	20	AAV59463	Banana fruit ripen
18	308.2	32.1	1118	21	AAV96233	cDNA encoding a ma
19	307	32.0	802	20	AAV9462	Banana fruit ripen
20	306	31.9	1013	21	AAV96231	cDNA encoding a ma
21	301.4	31.4	756	20	AAV24890	Rye chitinase-like
22	274.6	28.6	583	21	AAV96234	cDNA encoding a ma
23	260	27.1	768	20	AAV59466	Banana fruit ripen
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25	246	25.6	1077	21	AAV96230	cDNA encoding a ma
26	222.2	23.1	991	21	AAC41918	Arabidopsis thalia
27	203.4	21.2	2636	19	AAV49983	Floral organ-speci
28	194.4	20.2	730	20	AAV69465	Banana fruit ripen
29	186.6	19.4	1317	21	AAC48613	Nettle lectin cDNA
30	186.6	19.4	1317	22	AAC60211	Urtica dioica aggl
31	178	18.5	1010	11	AAQ06185	PR-Q cDNA cloned i
32	178	18.5	1020	10	AAV90845	Tobacco PR-Q gene
33	178	18.5	1020	20	AAV62809	Tobacco PR-Q gene
34	178	18.5	1020	20	AAV72995	PR-Q protein encod
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36	177.2	18.5	968	20	AAV62813	Tobacco PR-P gene
37	177.2	18.5	968	20	AAV81601	PR-P protein encod
38	173.8	18.1	1153	13	AAQ21007	Sequence encoding
39	173.8	18.1	1153	15	AAQ68352	Endochitinase prec
40	173.8	18.1	1160	13	AAQ21193	Sequence of chimera
41	173.8	18.1	1863	13	AAQ21191	Sequence of chimera
42	173.8	18.1	1863	15	AAQ74261	Tomato-tobacco end
43	169.2	17.6	965	12	AAQ12897	Petunia extracellu
44	169.2	17.6	966	18	AAT89951	Petunia hybrida ex
45	169.2	17.6	966	21	AAA58909	cDNA sequence enco

ALIGNMENTS

RESULT	1
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ID	AA24889 standard; cDNA; 954 BP.
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AC	AA24889;
XX	
DT	21-JUN-1999 (first entry)
XX	
DE	Rye chitinase-like protein CHT9 cDNA clone ch-9.
XX	
KW	CHT9; chitinase-like protein; antifreeze protein; AFP;
KW	winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW	transgenic plant; preservation; cryopreservation; tumour; therapy;
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PR	31-JUL-1997; 97US-0903872.

PN WO9007001-A.

XX 28-JUN-1990.

XX 13-DEC-1989; 89WO-US05501.

XX 16-DEC-1988; 88US-0285252.

XX (DUPO) DU PONT DE NEMOURS CO.

XX BROGLIE KE, BROGLIE RM;

XX WPI; 1990-224529/29.

XX P-PSDB; AAR05931.

XX Recombinant DNA contg. high level promoter and plant chitinase

XX gene - for transforming plants to over-express chitinase,

XX PT imparting resistance to phytopathogenic fungi.

XX PS Disclosure; ; pp; English.

XX Sequence encoding chitinase may be used to transform mono-

XX or dicotyledons to show increased resistance to fungal attack.

XX A high level promoter is used from CMV 35S or 19S complement,

XX NOS or OCS promoters of Agrobacterium opine synthetase gene,

XX the RUBISCO small unit or the chlorophyl A/B binding protein.

XX SQ Sequence 4704 BP; 1528 A; 783 C; 872 G; 1521 T; 0 other;

Query Match

Best Local Similarity 39.0%; Score 374.4; DB 11; Length 4704;

Matches 593; Conservative 0; Mismatches 281; Indels 30; Gaps 2;

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 Db 2461 aaactctcacgaacacacggggatggccactgcgcgcgcgcgcgcgcgcgcgcgcgc 2520
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 Db 2578 tccctgc 2637
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 Db 2698 tcgcacgtgactctgtct 2757
 QY 716 caccacgccttcgagc 775
 Db 2758 ccccccacacttctcccccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2817
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 Db 2818 tcgc 2877
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 QY 896 gcgacactccttgccgc 955
 Db 2938 gtgatctgttgagtggttatgttgcaacacacttgactctcagactccacttg 2997
 QY 956 cata 959
 Db 2998 gaaa 3001

RESULT 10

AAT79940

ID AAT79940 standard; cDNA; 879 BP.

XX AAT79940;

XX 10-OCT-1997 (first entry)

XX Chitinase coding sequence.

XX Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase;

XX fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.

XX Cucurbita pepo.

XX JP05163987-A.

XX 24-JUN-1997.

XX 14-DEC-1995; 95JP-0347367.

XX 14-DEC-1995; 95JP-0347367.

XX (NIHA) JAPAN ENERGY CORP.

XX (SEKI-) ZH SEXIYU SANGYO KASSEIKA CENTER.

XX WPI; 1997-380170/35.

XX P-PSDB; AAW24554.

XX Chitinase derived from pumpkin - used to protect plants against

XX pathogenic fungi

XX Claim 2; Page 2-4; 36pp; Japanese.

XX This sequence represents the coding sequence for the pumpkin chitinase.

XX Chitinase is an enzyme decomposing chitin (not present in plant cell

XX membranes) found in the cell membranes of fungi. Plants have this enzyme

XX to protect themselves from pathogenic fungi. Thus this enzyme can be used

XX to prevent plants from being infected with pathogenic fungi, and the

XX chitinase gene can be introduced into plants to improve their resistance

XX to diseases caused by fungi. As the amino acid sequence of the chitinase

XX does not have any region to be cleaved by ubiquitous peptidases in cells,

XX the chitinase produced by genetic recombination technology works for

XX various host cells and serves for plant immunity to confer disease

XX resistance on plants as the host.

XX Sequence 879 BP; 216 A; 221 C; 242 G; 200 T; 0 other;

XX SQ

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Query Match      38.5%; Score 369.2; DB 18; Length 879;
Best Local Similarity 65.2%; Pred. No. 1.8e-57;
Matches 583; Conservative 0; Mismatches 293; Indels 18; Gaps 2;

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QY 121 ttccggtttctgagcaccactccgaactactgcggcaccggtgcagaccagtgcaat 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ttccggtggtgcggcaacacgcagagtagtctgttaaaacaattgcccagaccagtgca 120

QY 181 ggtgcagcggcgccaccccggtacgggtacccgacccctccgagcgcgctctctcc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ccccccagtagcggcgccg-----ggcgcgcgcgcgcgagcgttggaagt 165

QY 241 attatctcgagtcgctctctcgcagcagatgctgacccgcagcagcggcgctgctg 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 atcatacgaagccctttacaataaactgctcaagtatagcagagtagctcgtatgcc 225

QY 301 gccaaaggggtttacaactacggcgcccttcgtgcggccgcacactggttctcgggttc 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 agtaatggattctatagatacaaatgctttactactgcgctcaactctctctctggttt 285

QY 361 gcgacacaggttagcaccgacgtcaagaagcggaggtgcccgttctctcgtcagact 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 ggtaccacggagatgctgctactctgtaaaogggaggttcagctttcttcggccaaact 345

QY 421 tccacagagacacggcggtggtggcgacggcgcccgcccgacggcccgccactcctgggtac 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 tctcatgaaccactggaggtgggtggtacggcaccggatggcccatatgctgggggtat 405

QY 481 tgttcaacagagcgcgcgcacactccgactactgcagcgcgagctgcactgcgca 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 406 tgttcaataggag---aaacaaagacgtatattgctcaccataccgcaactggcg 462

QY 541 tgtgcgcggcggaagaagtactctgcggcgcccgcccatccagatctcacacaactaac 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 463 tgtgctgctggcagaaatattacggcgcgtggacaaattcagctaacccataactaac 522

QY 601 tagggcgcgggcgagcgcacgacgacgacgacgacgacgacgacgacgacgacgacg 660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 tagggcgcgggtagggcgctaaatttgaatttgcgtgaacacccgtgattggtagcc 582

QY 661 tcggacgcgacgctgctgttaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 acggatccggtgtgtcattcaagacagccattgtgtgtgtgtgtgtgtgtgtgtgtgt 642

QY 721 aagccttcgagccacgacgtgatacagcggcggtgagcccttcggcgccgacccagcg 780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 aagcactgctgcatgattgtatcactggagatggcagccttcggcgccgacagt-gct 702

QY 781 gcggggaggggtgcctgggtacgtgtgatcaccaacatcatcaacgctgggctcagatgc 840
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Db 703 gcggggagagtgctgggtatggtgtcatcacaacatcatcaacgctgggctcagatgc 762

QY 841 gggcgcgggcagggcgccgtgtgcgcgacccggatcggtgttacaagcgtactgcgac 900
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 763 gggcggtgtgcgtagcagagtgctgtatagaaattgggttttacaagagtagctgtgat 822

QY 901 ctccttggtcgaactacgtgtgacaactggactgctacacaacaaagccggttc 954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 823 ttgttggcatcgctatggcaacaacttggattgcaacaatcaaaaggtctttc 876
```

RESULT 11

AAT79941

ID AAT79941 standard; cDNA; 998 BP.

XX

AC

XX

XX

```
DT 13-OCT-1997 (first entry)
XX Full length chitinase coding sequence.
XX Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase;
KW fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.
XX Cucurbita pepo.
XX Key Location/Qualifiers
FT CDS 1..879
FT /*tag= a
FT /product= chitinase
XX JP09163987-A.
XX 24-JUN-1997.
XX 14-DEC-1995; 95JP-0347367.
XX 14-DEC-1995; 95JP-0347367.
XX (NIHA ) JAPAN ENERGY CORP.
XX (SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
XX WPI; 1997-380170/35.
XX P-PSDB; AAW24554.
XX Chitinase derived from pumpkin - used to protect plants against
XX pathogenic fungi
XX Claim 3; Page 4-5; 36pp; Japanese.
XX This sequence represents the coding sequence for the pumpkin chitinase.
XX Chitinase is an enzyme decomposing chitin (not present in plant cell
XX membranes) found in the cell membranes of fungi. Plants have this enzyme
XX to protect themselves from pathogenic fungi. Thus this enzyme can be used
XX to prevent plants from being infected with pathogenic fungi, and the
XX chitinase gene can be introduced into plants to improve their resistance
XX to diseases caused by fungi. As the amino acid sequence of the chitinase
XX does not have any region to be cleaved by ubiquitous peptidases in cells,
XX the chitinase produced by genetic recombination technology works for
XX various host cells and serves for plant immunity to confer disease
XX resistance on plants as the host.
XX Sequence 998 BP; 269 A; 238 C; 258 G; 233 T; 0 other;
```

```
Query Match      38.5%; Score 369.2; DB 18; Length 998;
Best Local Similarity 65.2%; Pred. No. 1.8e-57;
Matches 583; Conservative 0; Mismatches 293; Indels 18; Gaps 2;

QY 61 gagcaatgcgctcgcagcggcgccgagcgtgcccgaactgctctctgcagcaag 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 gagcaatgtagcgagcgaatgagcgtctctgcccgaactgctctctgcagcag 60

QY 121 ttccggtttctgagcaccactccgaactactgcggcaccggtgcagaccagtgcaat 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ttccggtggtgcggcaacacgcagagtagtctgttaaaacaattgcccagaccagtgca 120

QY 181 ggtgcagcggcgccaccccggtacgggtacccgacccctccgagcgcgctctctcc 240
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Db 121 ccccccagtagcggcgccg-----ggcgcgcgcgcgagcgttggaagt 165

QY 241 attatctcgagtcgctctctcgcagcagatgctgacccgcagcagcggcgctgctg 300
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Db 166 atcatacgaagccctttacaataaactgctcaagtatagcagagtagctcgtatgcc 225

QY 301 gccaaaggggtttacaactacggcgcccttcgtgcggccgcacactggttctcgggttc 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 agtaatggattctatagatacaaatgctttactactgcgctcaactctctctggttt 285

QY 361 gcgacacaggttagcaccgacgtcaagaagcggaggtgcccgttctctcgtcagact 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


Db	286	ggtaccacgaggaatctgctactactogtaaacgggagcttgagcttctctcggccaact	345
QY	421	tccacgagacgacccggggtggccagacggcgccgacggccctactcctcgggctac	480
Db	346	tctctgaaccactggagggtgggtactacggcacggatggcccatatcgtcgggatat	405
QY	481	tgotttaaccagagacggcgcccaactccgactactgcacgcccagctcgcagtgcca	540
Db	406	tgcttcataaggag--agaaaccagaagcttatctgtccactaacagagaatggcg	465
QY	541	tgtgcgcgggcaagaagtacttcggcgcgggcccatccagatctcacacaactacaac	600
Db	463	tgtcgtcgtggccagaaaattacggcctggaccaattcagtaaacccataactacaac	522
QY	601	tacggcgccggggcaggccatcgggcaacggacctgctcaaacaccggaccttgggcg	660
Db	523	tacggcgacgggtaggcgctaaattgaatttgctgaacaacctgatttggtagcc	582
QY	661	tcggacgcaccctgcgttttaagacgggtgtgctctgatatgacgcgaataccgc	720
Db	583	acggatccggttctgattcaaggacgccatttgctctggatgacacacgaagaaac	642
QY	721	aagccttcgagcacgactgatcacgggcgggtggagccctcgggcgcgcacaggcg	780
Db	643	aagccatcgtgccatgatgtatactggagatggagcttcggcgcgcgacagtgt	702
QY	781	gcggggagaggtgacctgggtacggttgataccacaacatcataacgggtcgaagtgc	840
Db	703	gccgggagagtgcctgggtatgggtcatcaacaacatcataatggtgggctcgaagt	762
QY	841	ggcgcgggcgaggacggcgttcgcgcacccgatcgggtctctacaagcgctactcgac	900
Db	763	ggcggtggtccgatagcaagtgctgatagaaatgggttttacaataaggctactgtat	822
QY	901	ctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttc	954
Db	823	tgtgtggcactcggctatggcaacaactctggattggaacaatcaaaagctcttc	876

RESULT 12

AL030132	
AAT33325	
ID	AAT33325 standard; DNA; 1225 BP.
XX	
XX	
AC	AAT33325;
XX	
DT	18-OCT-1996 (first entry)
XX	
DE	American elm chitinase-like protein coding sequence.
XX	
KW	Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi;
KW	dutch elm disease; E. coli; chitinase-like protein;
KW	fungal infection; ss.

OS American elm.

AA	Key	Location/Qualifiers
FH		

sig_peptide

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/*tag=
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FT mat_peptide 151..10

$$\frac{\text{FT}}{\text{FT}} = \frac{\text{FT}}{\text{FT}}$$

FT CDS 88..1041

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FT
/*tag= c

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FT
/product=

FT polyA_signal 1147..1151

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FT      /*tag= d
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FT polyA_signal

LE

53

PD	23-JUL-1996.	
XX		
XX	04-AUG-1994;	94US-0286020.
XX		
XX	04-AUG-1994;	94US-0286020.
XX		
XX	(UNMS) UNIV MICHIGAN STATE.	
XX		
XX	Hajela RK, Sticklen MB;	
XX		
DR	WPI: 1996-353879/35.	
DR	P-PSDB; AAW00186.	
XX		
PT	Isolated chitinase gene derived from an American elm - used to	
PT	obtain prods. for inhibiting fungal infection of plants	
XX		
PS	Claim 1; Fig 1; 12pp; English.	
XX		
CC	This sequence represents the cDNA clone pHS2, which encodes a protein	
CC	having chitinase-activity derived from american elm. This protein	
CC	inhibits the fungus Ophiostoma ulmi, the causative agent of dutch	
CC	elm disease. The clone pHS2 may be used to transform E. coli cells	
CC	for the recombinant production of the chitinase-like protein. The	
CC	protein may be used in a composition to inhibit fungal infection of	
CC	elm trees.	
XX		
SQ	Sequence 1225 BP; 322 A; 277 C; 313 G; 313 T; 0 other;	

ID	Name	Accession	Length	Score	DB	Indels	Mismatches	Gaps
AAT89952	standard; cDNA; 1152 BP.		36.2%	63.2%	DB 18;	0	314	24
XX	AAT89952;							
XX	11-MAR-1998 (first entry)							
XX	Nicotiana sp. intracellular chitinase cDNA.							
DE	Intracellular chitinase; antifungal; synergism;							
KW	beta-1,3-glucanase gene; tobacco; ss.							
XX	Nicotiana sp.							
OS	Key	Location/Qualifiers						
XX	CDS	10..984						
FT	/tag= a							
FT	sig_peptide	10..78						
FT	mat_peptide	79..981						
FT	/tag= b							
FT	/tag= c							
FT	/product= intracellular_chitinase							
XX	US5670706-A.							
XX	23-SEP-1997.							
XX	19-APR-1993; 93US-0047413.							
XX	29-JAN-1991; 91US-0647831.							
XX	(MOGE-) MOGEN INT NV.							
PA	(OYLE-) RIJKSUNIV LEIDEN.							
XX	Bol JF, Cornelissen BJC, Linthorst HJM, Melchers LS;							
PI	Meutenhoff EJS, Sela-buurlage MB, Van ROEKEL JSC;							
PI	Vloemans AA, Woloshuk CP;							
DR	WPI; 1997-479536/44.							
DR	P-PSDB; AAW31297.							
XX	Fungal-resistant transgenic plants - containing genes encoding							
PT	intracellular chitinase and beta-1,3-glucanase							
XX	Example 4; Fig 2; 42pp; English.							
CC	This cDNA sequence encodes an intracellular chitinase which is used							
CC	to construct a transgenic plant in a novel method to produce plants							
CC	resistant to fungal attack. Such transgenic plants expressing an							
CC	intracellular plant chitinase gene and a plant beta-1,3-glucanase gene							
CC	within its tissues are predicted to exhibit improved resistance to							
CC	pathogenic fungi. Such genes should be operably linked to promoters and							
CC	terminators and optionally a gene encoding a selectable or screenable							
CC	trait. Plants that overexpress the chitinase and glucanase genes							
CC	exhibit a synergistic antifungal effect.							
XX	Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;							
SQ	Query Match	36.2%; Score 347.6; DB 18; Length 1152;						
XX	Best Local Similarity	63.2%; Pred. No. 1.2e-53;						
XX	Matches 580; Conservative 0; Mismatches 314; Indels 24; Gaps 2;							
QY	45	cgtgctgcagcagcaatcgctgcagccggcgccggcgacgtgccccaactg 104						
Dd	63	ctctctgcctgcggagaacaattggttcgcaaggcgagggtgcgcttgctcccg 122						
QY	105	ctctctgcagcaaatgctggttttgcgcaccacctccgaactactgcggcacggc-- 162						
Dd	123	tctctgcagcaaaatttggttggttgtaaacaccaataactactattgtgccctggcaa 182						
QY	163	-tgcagagccagtgcagtgcgcagcgccgacccccgggtaccgggtaccgcccctc 221						

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:27:02 : Search time 142.45 seconds
(without alignments)
1526.282 Million cell updates/sec

Title: US-09-534-229C-8

Perfect score: 960

Sequence: 1 atgagaggagtggtggtggt.....accaaaggcgttcgcatag 960

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCOTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614.6	64.0	1151	1	US-07-704-288C-2
2	614.6	64.0	1151	1	US-08-093-372-1
3	614.6	64.0	1151	1	US-08-379-259-2
4	513.6	53.5	1002	1	US-08-457-797A-9
5	513.6	53.5	1002	1	US-08-812-025-9
6	513.6	53.5	1002	4	US-09-138-873A-9
7	358	37.3	1225	1	US-08-286-020-1
8	358	37.3	1225	1	US-08-603-919-1
9	349.2	36.4	943	2	US-08-475-427-15
10	349.2	36.4	943	2	US-07-842-165-15
11	347.6	36.2	1152	1	US-08-047-413-10
12	347.6	36.2	1152	3	US-08-229-050-10
13	347.6	36.2	1152	3	US-08-801-563-10
14	289.6	30.2	905	2	US-08-475-427-14
15	289.6	30.2	905	2	US-07-842-165-14
16	186.6	19.4	1317	3	US-07-791-931-1
17	178	18.5	1020	1	US-08-181-271A-7
18	178	18.5	1020	1	US-08-449-315-7
19	178	18.5	1020	1	US-08-444-803-7
20	178	18.5	1020	1	US-08-449-043-7
21	178	18.5	1020	1	US-08-456-265A-7
22	178	18.5	1020	1	US-08-455-416-7
23	178	18.5	1020	1	US-08-455-244-7
24	178	18.5	1020	1	US-08-454-876-7
25	178	18.5	1020	2	US-08-457-364-7
26	178	18.5	1020	2	US-08-456-262-7
27	178	18.5	1020	2	US-08-456-240-7

28	178	18.5	1020	2	US-08-455-736-7	Sequence 7, Appli
29	178	18.5	1020	2	US-08-971-217-7	Sequence 7, Appli
30	178	18.5	1020	4	US-09-350-600-7	Sequence 7, Appli
31	177.2	18.5	968	1	US-08-181-271A-12	Sequence 12, Appl
32	177.2	18.5	968	1	US-08-449-315-12	Sequence 12, Appl
33	177.2	18.5	968	1	US-08-444-803-12	Sequence 12, Appl
34	177.2	18.5	968	1	US-08-449-043-12	Sequence 12, Appl
35	177.2	18.5	968	1	US-08-456-265A-12	Sequence 12, Appl
36	177.2	18.5	968	1	US-08-455-416-12	Sequence 12, Appl
37	177.2	18.5	968	1	US-08-455-244-12	Sequence 12, Appl
38	177.2	18.5	968	1	US-08-454-876-12	Sequence 12, Appl
39	177.2	18.5	968	2	US-08-457-364-12	Sequence 12, Appl
40	177.2	18.5	968	2	US-08-456-262-12	Sequence 12, Appl
41	177.2	18.5	968	2	US-08-456-240-12	Sequence 12, Appl
42	177.2	18.5	968	2	US-08-455-736-12	Sequence 12, Appl
43	177.2	18.5	968	2	US-08-971-217-12	Sequence 12, Appl
44	177.2	18.5	968	4	US-09-350-600-12	Sequence 12, Appl
45	173.8	18.1	1153	2	US-08-475-427-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-07-704-288C-2
; Sequence 2, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 64.0%; Score 614.6; DB 1; Length 1151;
Best Local Similarity 80.3%; Pred. No. 1.6e-112;
Matches 773; Conservative 0; Mismatches 179; Indels 11; Gaps 4;

[illegible]

RESULT 2

RECEIVED
US-08-093-372-1

; Sequence 1, Application US/08093372

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QY 357 ctccgagacacagtagcaccagcgtcgaagagcgaggtggccggtctccgtcga 416
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Db 411 CTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
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QY 417 gacttccacagagacgacgagcggtggggtggccgagcgcccgagcgccctactcctgggg 476
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Db 471 GAGTCTCCACGAGACCGCGCGCGGTGGGGGAGCGCGCGCGCGCGCGCGCGCGCG 530
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QY 477 ctactgttcaaccagag--cgcgcgcaacctcgactactgacgacgagcgtcga 533
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 531 CTACTGCTTCAAGAGAGAGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 590
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 534 gtggccatgtgcgcggtggggaagtagtcttcggcgcggtgggccccatccagatctcacaca 593
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 591 GTGGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 650
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 594 ctacaactacggtcggtggggtggggtggggtggggtggggtggggtggggtggg 653
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 654 tggggtcgagcgagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 713
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Db 711 CGTGGGCTGTGACGCCACCGTCTCTTTCGACACGCGCGCGCGCGCGCGCGCG 770
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QY 714 atacccaactctcgagcgacgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 773
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 771 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 830
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 774 ccaggcggtgggaggtgctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 833
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Db 831 CCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 890
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 834 cgagtgcggtgcggtgcggtgcggtgcggtgcggtgcggtgcggtgcggtgcggt 893
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Db 891 GGAGTGGCGCATGCGCGAGGACGATCGATCGCGCGCGCGCGCGCGCGCGCG 950
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 894 ctgcgacctctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 953
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 951 CTGCGGACATCTCGGCGTCACTACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1010
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QY 954 cgc 956
|||
Db 1011 GGC 1013

RESULT 3
us-08-379-259-2
; Sequence 2, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-08-379-259-2

Query Match. 64.0%; Score 614.6; DB 1; Length 1151;
Best Local Similarity 80.3%; Pred. No. 1.6e-112;
Matches 773; Conservative 0; Mismatches 179; Indels 11; Gaps 4;

QY 1 atgagagagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 57
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Db 55 ATGAGAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 114
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QY 58 gccagagcaatgctgcgagcggtggtggtggtggtggtggtggtggtggtggtggt 117
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Db 115 GCGGAGCAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 174
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QY 118 aagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 177
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Db 175 CAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234
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QY 178 -aatggtgcagcggtggtggtggtggtggtggtggtggtggtggtggtggtggt 236
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Db 235 TCGGCGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 290
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QY 237 ctccattatctgcgagtcgtctcttcgacacagatgctgctgcacgcgacgacggtg 296
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Db 291 GTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 350
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QY 297 cctggccaaggggtctacaaactacggtggtggtggtggtggtggtggtggtggtg 356
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Db 351 CCGGCGCAGCAACTTCTACACCTACGAGCGCTTCTGTCGCGCGCGCGCGCGCGCG 410
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QY 357 ctgcgaccacaggttagcaccgagctgaagagcgaggtggtggtggtggtggtggt 416
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 CTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 417 gacttccacagagacgacggtggtggtggtggtggtggtggtggtggtggtggtg 476
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Db 471 GACGTCCACAGACACCGCGCGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 530
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QY 477 ctactgttcaaccagag---cgcgcgcaacctcgactactgacgacgagcgtcga 533
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Db 531 CTACTGCTTCAAGGAGGAGAGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 590
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QY 534 gtggccatgtgcgcggtggggaagtagtcttcggcgcggtgggccccatccagatctcacaca 593
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Db 591 GTGGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 650
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QY 594 ctacaactacggtcggtggggtggggtggggtggggtggggtggggtggggtggg 653
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 651 CTTCAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 710
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QY 654 tgtggcggtcgagcgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 713
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 248 CCGCCCTCCGGGCTTCGGCACCACACCGGACGCGCCGACGCCAGAGCGGTGGCCG 307
QY 404 cgtctcgtcagactccacagacacacgagcggtgacgagcgagcgagcgagc 463
Db 308 CCTCTCTAGCAGACACTCCACAGACACACCGCGGTGGGCGATGACCCGAGCGGG 367
QY 464 cctactctggggtactgttcaacacagagcgcgcgccactccgactactgcacgc 523
Db 368 CCTTCGCGCTGGGCTACTGTTCAAGCAGGACGCGCGCTCTCTCGACTACTGCACCC 427
QY 524 cgaagctcgaagtgccatgtgcccgggcaagaagtacttcggggcgggcccatcaga 593
Db 428 CGAGCGCACAAATGGCGCTGGCCCCGGGAGAGCGCTACTACGCGCGGGCCAAATCCAGC 487
QY 584 tctcacacactacaactacgagcgcggggagggcgagccatcgcaacgacgtctcaaca 643
Db 488 TCTCCACAACTACAATATGGACCTGCCGCGGGCCATCGGGGTGATCTCTGGCCA 547
QY 644 accggacacttggtggcgagcgagcagcggtgctgttaagacggcggtgtgttctgga 703
Db 548 ACCCGGACCTGTGGTGGCCAGGACGCCACTGTGGGCTTTAAGACGGGCATCTGTTCTGGA 607
QY 704 tcaacgcgaatcaccaagccttcagcaacgacgtgacgtgacgagcggtgagccct 763
Db 608 TGACGGCGGACCGCCCAAGCCATCGAGCATGCTGTGATCGCGCGCCAGTGGAGCCGT 667
QY 764 cggcgccgaccagggcggggaggggtgctgggtacggtgacgtgacacacatcatca 823
Db 668 CAGGGGCTGACCGCGCGGACGAGCGGGTGCCTGGTGTGATCACCACATCATCA 727
QY 824 acggtggctcagtgagggcgcgggcagcagcgcggtgctgcgcgacggatcggttct 883
Db 728 ACGGCGGGATCGAGTGGGTGACGGCAGACACCGCGCTCGCGCGATCGAATCGGGTTT 787
QY 884 acaagcgactcgactcctctggtgagtcagtcaggtgacacactggactgtacaacc 943
Db 788 ACAGCGCTACTGTGATCATCTCTCGGCTTGGCTACGGCAACAACTCGATTGCTACAGCC 847
QY 944 aaagcgcttcgcata 959
Db 848 AGAGACCTTCGCGCTA 863

RESULT 7

US-08-286-020-1
; Sequence 1, Application US/08286020
; Patent No. 5539095
; GENERAL INFORMATION:
; APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
; TITLE OF INVENTION: A Chitinase cDNA Clone From a
; TITLE OF INVENTION: Disease Resistant American
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS 5.00
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,020
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5539095e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1225
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Ulmus Americana
; STRAIN: NPS 3-487
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE: N/A
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: chitinase encoding DNA
; LOCATION:
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: DNA needed for chitinase
; OTHER INFORMATION: in elm.
; PUBLICATION INFORMATION:
; US-08-286-020-1

Query Match 37.3%; Score 358; DB 1; Length 1225;
Best Local Similarity 64.0%; Pred. No. 3e-62;
Matches 575; Conservative 0; Mismatches 290; Indels 33; Gaps 1;
QY 58 gccgagcaatcgcgctgcgagcgcgggcgagctgcccccaactgcctctgtgcagc 117
Db 148 GCAGAGCAATGTGGAGCCAAAGTGGGGTGCAGTGTGTCCCGTTGGGCTCTGTGTCAGC 207
QY 118 aadtgggttttcgagcaccactccgactactgagcaccggtcgccagagccactgc 177
Db 208 AAATTGGGTGGTGGGAGCACAACAGTACTGTGTGATGCTGCCAAGCAATGT 267
QY 178 aatgggtcgagcgcgccaccccggtaccggtaccgacccctcccgcgcggtctcc 237
Db 268 GCGGCGAGCGTAGCGAT-----GACATTGGC 294
QY 238 tccattatctcgagtcgtctcttcacagatgctgtgcacgcaacgagcggtgc 297
Db 295 GGTCTCATATCAAGCTCCGCCCTTTAATGACATGCTTAAGCATCGTAACGACGGTGTGT 354
QY 298 ctggcgaaggggtttctacaactacgagcgcccttcgctcccgcccaactcgttctcgggc 357
Db 355 CCGCCCAAGGGGTTTTACACCTATGATGCTTTTATTCGGCTGCCAAGGCTTTCCTCGCA 414
QY 358 ttgcgcaccacaggtagcaccgacgtcaagaagcgcgaggtggcggttctcgtcag 417
Db 415 TTGGCTCCACCGCGGATGATACCCCGTAAGAGGAGATTGCTGCTTTCTTAGGTCAA 474
QY 418 acttccacgagacgagcggtgtgcccagcgccccgacgccccctactcctggggc 477
Db 475 ACTTCCCATGAACACTACAGGTGGGTGGGCAAGTGCACCCGCGGTCCATCTCTTTGGGA 534
QY 478 tactgttcaaccagagcgcgccacactccgactactgcacgcccagctcagatgg 537

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Db 535 TACTGCTACATAGGAGCAAAACCTCTCCGATTATTGTTCTTTAGTCTACTTGG 594
QY 538 ccattgcccgggcaagaagtaactcgggcggcgcccaatccagatctcaacaactac 597
Db 595 CTTTGCTCTCCGAAAGAGATACITTTGGCGGTGCCAATCAACTCTCTCGGAACATC 654
QY 598 aactacggccggcgggcgagggccatcgccacgcgcctctcaacaacccggaccttg 657
Db 655 AACTATGGACAGTGGGAAGGCCATAGAGCAACACCTATTAAACACCTGATCTGTA 714
QY 658 gggcgagcagcagcgtgctgttaagacggcggtgtgtgttctgagtcgacgcaatca 717
Db 715 GCAACTGACCTCTCATTTCTTCAAAACGGCTTATGTTCTGGATGACCCACAGTCA 774
QY 718 ccaagccttcgagcagcagcgtgatcacggcgccggtgagccctcgggcccgaccag 777
Db 775 CCNAAAGCCCTCGGCATGACGTATCACCGGAAGTGGAGTCTTCCGGCACCCAG 834
QY 778 gggcgggggggtgctgggttacggtgtgatccaaacatcatcaacgggtgggtcgag 837
Db 835 TCGGCGCGCGAGTTCGGGCTACGGCGTATCACCAACATTATCAACGGTGGATAGAA 894
QY 838 tcggggcgggcagcagcggcggtgctgcggcagcgatcggttctacaagcgctactgc 897
Db 895 TCGGGGAAGGTCAGTCTCCTCAGGTGGGATCGGATTGGATTCTACAAAGGACTCT 954
QY 898 gacctctctggcgctcagctacggtgacacccctggagctgtacacaaaggcgctcg 955
Db 955 GATATCCTTAGAGTTGGCTATGGGAACAATCTTGATGCTATACCAAGAGGCTTTTG 1012

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RESULT 8

US-08-603-919-1

; Sequence 1, Application US/08603919

; Patent No. 5728382

; GENERAL INFORMATION:

; APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela

; TITLE OF INVENTION: A Chitinase cDNA Clone From a

; TITLE OF INVENTION: Disease Resistant American

; TITLE OF INVENTION: Elm Tree

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ian C. McLeod

; STREET: 2190 Commons Parkway

; CITY: Okemos

; STATE: Michigan

; COUNTRY: USA

; ZIP: 48864

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage

; COMPUTER: Acer

; OPERATING SYSTEM: MS-DOS 5.00

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/603,919

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Ian C. McLeod

; REGISTRATION NUMBER: 20,931

; REFERENCE/DOCKET NUMBER: MSU 4.1-207

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 347-4100

; TELEFAX: (517) 347-4103

; TELEX: No 5728382e

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1225

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

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; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Ulmus Americana
; STRAIN: NPS 3-487
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE: N/A
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: chitinase encoding DNA
; LOCATION:
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: DNA needed for chitinase
; OTHER INFORMATION: in elm.
; PUBLICATION INFORMATION:
US-08-603-919-1

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Query Match          37.3%; Score 358; DB 1; Length 1225;
Best Local Similarity 64.0%; Pred. No. 3e-62;
Matches 575; Conservative 0; Mismatches 290; Indels 33; Gaps 1;

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QY 58 gccgagcaatcggtcgcgagcgcgggcgagcggtgcccacactgcctgtctgcagc 117
Db 148 GCAGAGCAATGTGGAAGCCAGCTGGGGGTGCAGTGTGCCGTGGGGCTCTGCTGCAGC 207
QY 118 aagttcggttctcgccacacctccgactactggtggcaccgggtgcagagccagttgc 177
Db 208 AAATTTGGTGGTGGGAGCACAACAGAGTACTGTGTGATGGGTGCCAAGCCCAATGT 267
QY 178 aatgctcgcgcgcgcccggtaccggtaccggtaccggtaccggtaccggtaccggt 237
Db 268 GCGGCGAGCGGTAGCGAT-----GACATTGGC 294
QY 238 tccattatctgcagtcgtctcttcgaccagatgctgtgcacgcgaacgacgcggtgc 297
Db 295 GGTCTCATATCAAGCTCCGCTTTAATGATGATGCTTAAGCATCGTAACGACGCTGGTTGT 354
QY 298 ctggccaaagggttctacaactacgcgccttcgtcgccgcgcgaactcgttctcgggc 357
Db 355 CTTGCCAAGGGGTTTACACCTATGATGCTTTATTTGCGGCTGCCAAGGCTTCCCTGCA 414
QY 358 ttccgcacacacaggttagcaccgcgcgtcaagaagcgaggtggcgcggttctcgtctcag 417
Db 415 TTTGGCTCCACCGCGGATGATACCAACCCGTAAGAGGAGATTGCTGCTTTTACTAGTCAA 474
QY 418 acttcccaagacagcagcgcggggtggcgacgagcgcgcccgccctactcctctggggc 477
Db 475 ACTTCCCATGAAACTACAGGTGGGTGGGCAAGTGCAACCGAGGTCATACACTTTGGGGA 534
QY 478 tactgttcaaccagagcgcgcgccacctccgactactgacgcgaggtcgagttgg 537
Db 535 TACTGCTACATAGGAGCAAAACCTCTTCCGATTATTGTTCTTTAGTCTACTTGG 594
QY 538 ccattgcccgggcaagaagtaactcgggcggcgcccaatccagatctcaacaactac 597
Db 595 CTTTGCTCTCCGAAAGAGATACITTTGGCGGTGCCAATCAACTCTCTCGGAACATC 654
QY 598 aactacggccggcgggcgagggccatcgccacgcgcctctcaacaacccggaccttg 657
Db 655 AACTATGGACAGTGGGAAGGCCATAGAGCAACACCTATTAAACACCTGATCTGTA 714
QY 658 gggcgagcagcagcgtgctgttaagacggcggtgtgtgttctgagtcgacgcaatca 717

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GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: EIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842.165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-842-165-15

Query Match 36.4%; Score 349.2; DB 2; Length 943;
Best Local Similarity 63.3%; Pred. No. 1.6e-60;
Matches 581; Conservative 0; Mismatches 313; Indels 24; Gaps 2;

QY 45 cgtgtctgcacgcgcgaatcggtctcgaggccgcggcgagctgaccccaactg 104
DB 12 CTTCTGCTCGGCAGACAAATGGTGGTAAACCAATGACTATTGGGCCCTGGCA 131
QY 105 cctctgctgcagcaagttcggtttctgcggcaccacctccgactactcggcacccgcg-- 162
DB 72 TCTCTGCTGCAGCAAAATGGTGGTAAACCAATGACTATTGGGCCCTGGCA 131
QY 163 tgcagagcagtgcaatggctcagcggcgccaccgcgggtaccggtacacccctc 221
DB 132 TTGCCAGAGCCAGTCCCTCGTGGTCCCA-----CACCACCCGG 170
QY 222 cggcgccggtctcctccattatctcagtcgctcttcacacagatgctgctcacg 281
DB 171 TGGTGGGATCTCGGCAGTATCATCAAGTTCCATGTTGATCAGATGCTTAAGCATCG 230
QY 282 caacgacggtcgctcgtggcgaaggggtttacacactacggtcgtcgcgcgcgcgc 341
DB 231 CAACGATATGATGCCAAGGAAGGATTCACAGTTACATGCTTTATCAATGCTGC 290
QY 342 caactcgttctcgttctcgttcgacacacaggttagcaccgacgtcaagaagcgggtg 401
DB 291 TAGGCTCTTTCTCGCTTGGTGGTACTAGTGGTATACCACTGCCCGCTAAAGAGAAATCG 350
QY 402 cgcgttctcgtcgtcagacttccaccagacgacgacggcggttgccgacggtccgcgacg 461

DB 351 GGCTTTCTTGGCCCAACCTCCCATGAAACTACAGSAGATGGCAACAGCACCAGATGG 410
QY 462 cccctactcctgggtgactgcttcaaccagagcgcgccacactcgcactaactgac 521
DB 411 TCCATACGCGTGGGTTACTGCTGGCTTAGAGAAACAAGTAGCCCCGGGACTACTGTAC 470
QY 522 gcgagctcgcagtgccatgtgcggcggaagtaacttcggcgcgccgcatcca 581
DB 471 ACCAAGTGGTCACTGGCTTGTGCTCCTGGTGGGAATAATTTTCGACGAGGCCCATCCA 530
QY 582 gatctcacacaactacaactacggcgcgggcgagccatcggcacgcgacctgctcaa 641
DB 531 AATTTACACAACTACAACTAGGACCTTGTGGAAGAGCCATAGGAGTGGACCTCTATAA 590
QY 642 caaccggacacctgtggcgctggagcgcgacgctgcttttaagacggtgtgtgtctg 701
DB 591 CAATCCTGATTAGTGGCCACAGATCCAGTAATCATTCATCAAGTCAAGTCAAGTCAAGTCA 650
QY 702 gatgacgcgcgaatcaccccaagccttcgagccacgacgtgacggtgagccg 761
DB 651 GATGACTCTCAATCACCAAAACCTTCTTGCACGATGTATCATTTGGAAGATGGCAAC 710
QY 762 ctggggcgccgacagggcgggggaggggtgctgggtacgggtgacacacacatcat 821
DB 711 ATCGTCTGCTGACCGCGCAGCCAAATCGTCTCCCTGGATTGCTCATCACGAACATCAT 770
QY 822 caacggtggtcgagtcggcgcgcgcgagcggcgctgctgcgcgacccggtcggtt 881
DB 771 CAATGGTGGCTTGGAAATGGTGGTGGCAGTCACTGACCAAGGTCAGGATCGCATTTGGGT 830
QY 882 ctacaagcgtactcgacacctccttggcggtcagctacggtgacacacctggactgataca 941
DB 831 TTACAGGAGGTATTGCTGTTGGTGTAGTCTCTGTGTGACAATCTTGATTGGGAAA 890
QY 942 ccaaaaggcgttgcgata 959
DB 891 CCAGAGGTCTTTTGGAAA 908

RESULT 11
US-08-047-413-10
; Sequence 10, Application US/08047413
; Patent No. 5670706
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Seia-Buurilage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/047.413
; FILING DATE: 19-APR-1993

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/clone_lib="Hordeum vulgare 20 DAP spike EST library
HvCDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLP"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 117 a 261 c 219 g 108 t
ORIGIN

Query Match 60.2%; Score 578.4; DB 11; Length 705;
Best Local Similarity 94.7%; Pred. No. 1.1e-98;
Matches 610; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
QY 1 atagaggatttggtggtggccatgctgcccggcgcttcctccgtgtctgcgcaagc 60
Db 61 ATGAGAGGACTTGTGGTGGTGGCCATGCTGCCGCGGCCCTTCGCCGTAATCTGTACAGCC 120
QY 61 gagcaatgctgcgagcgccggcggaagctgcccccaactgcctctgtcagcaag 120
Db 121 GAGCAGTGGGCTTCGACAGCGCGGGGACGTGCCCAACTGCTCTGCTGCAGCAGG 180
QY 121 ttccgtttctgcggcaaccactccgactactgctggcaccggctgcagagcagtgcaat 180
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Db 241 GGTGTCGGCGCGCGCGCACCCCGGTACCGGTACCGCCGCCCTTCGGCGCGCGGTGCC 300
QY 238 tccattatctcgagtcgctctcttcgaccagatgctgctgcacgcacacgagcggtgc 297
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QY 298 ctggccaagggtttctacactacggccttcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgc 357
Db 361 CAGGCCAAGGGGTCTTACAACTACGGCGCCTTCGTGCGCGCGCGCGCGCGCGCGCGCG 420
QY 358 ttgcgaccacaggttagcaccgagctcaagaagcgagagtgcccgcttcctcctcag 417
Db 421 TTCGACACACGGGTGACCCGACGTGAGGAGCGGAGGTGGCGCGCTTCCTCGCACAG 480
QY 418 acttccacagagacgacggcggtggtgcccagcgcgcccgacggccctactcctcgtgggc 477
Db 481 ACCTCCACAGACACCGCGCGGTGSCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 478 tactgttcaaccagagcgcgccacactccgactactgacgcgcgcgcgcgcgcgcgcgcgc 537
Db 541 TACTGTCTCAACAGAGCGCGCGCGCACTCCGACTACTGCACGCGAGCTCGCAGTGG 600
QY 538 ccattgtcgccgggcaagaagtacttcggcgcgcgcccgccatccagatctcacacaactac 597
Db 601 CCGTGGCGCGCGCGCGAGAGTACTTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 598 aactacgggcggcggggagggccatcggaaccgacactgctcaa 641
Db 661 AACTACGGCGCGCGCATGCGGGGCCATGCGGGCGCGACCTGCTCAA 704

RESULT 2
BG367616 711 bp mRNA EST 08-MAR-2001
LOCUS HVSMEI0012P08f Hordeum vulgare 20 DAP spike EST library HvCDNA0010
DEFINITION (20 DAP) Hordeum vulgare cDNA clone HVSMEI0012P08f, mRNA sequence.
ACCESSION BG367616
VERSION BG367616.1 GI:13256715
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 711)
Wing, R., Close, T. J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
J., Sasaki, C., Schwartzbeck, J., Simmons, J., Choi, D. W., Main, D., and
Wood, T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCCTACTAAGG
High quality sequence stop: 678.
Location/Qualifiers
1..711
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEI0012P08f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HvCDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLP"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 118 a 260 c 224 g 109 t
ORIGIN

Query Match 59.7%; Score 572.8; DB 11; Length 711;
Best Local Similarity 94.5%; Pred. No. 1.2e-97;
Matches 616; Conservative 0; Mismatches 32; Indels 4; Gaps 2;
QY 1 atagaggatttggtggtggccatgctgcccggcgcttcctccgtgtctgcgcaagc 60
Db 60 ATGAGAGGACTTGTGGTGGTGGCCATGCTGGCGCGGCCCTTCGCCGTAATCTGTACAGCC 119
QY 61 gagcaatgctgcgagcgcgcgcgagctgcccccaactgcctctcctcgtcagcaag 120
Db 120 GAGCAGTGGGCTTCGACAGCGCGGGGACGTGCCCAACTGCTCTGCTGCAGCAGG 179
QY 121 ttccgtttctgcggcaaccactccgactactgcggaaccggctgcagagcagtgcaat 180
Db 180 TTCGGCTTCTCGCGCTCCACCTCCGACTACTGGGGCACCGCGCTGCCAAAGCCAGTGCAAC 239
QY 181 ggcct---gcagcgcgccaccggctaccggtaccggtaccacccctccggcgcgctctcc 237
Db 240 GGTGCGCGCGCGCGCGCACCCCGGTACCGGTACCGCCGCCCTTCGGCGCGCGGTGCC 299
QY 238 tccattatctcgagtcgctctcttcgaccagatgctgctgcacgcacacgacgcgcgtgc 297
Db 300 TCCATTATCTCGCAGTCGCTCTTCGACCAACATGCTGTGACCCCAACAGATGCGGGGTGC 359
QY 298 ctggccaagggtttctacactacggcgcttcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgc 357
Db 360 CAGGCCAAGGGGTCTTACAACTACGGCGCCTTCGTGCGCGCGCGCGCGCGCGCGCGCG 419
QY 358 ttgcgaccacaggttagcaccgagctcaagaagcgaggtgcccgcttcctcctcag 417
Db 420 TTCGACACACGGGTGCGCGCTCCGACTACTGGAGCGCGAGGTGGCGCGCTTCCTCGCACAG 479
QY 418 acttccacagagacgacggcggtggtgcgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 476
Db 480 ACCTTCCACGAGACACCGCGGGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 539


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Qy 477 ctactgtctcaacaggagcgcgccacactccgactactgacgcgcgagctcgagtg 536
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Qy 537 gccatgtgcgcggcggaagaagtacttctggcgcgggcccatccagatctcacaaacta 596
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Db 600 GCGGTGCGCGCGCGCAAGAGTAGTCTTCGGCGCGGGGCCATCCAGATCTCCCAACTA 659
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Qy 597 caactacggcgcgggcgagcgccatcgccacgcagctgtctcaacaaccg 648
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Db 660 CAACTACGGCGCGGAGCGCGGCATCGCGCGGACCTGCTCAACACCCG 711
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RESULT 3
LOCUS BE705117/c 681 bp mRNA EST 12-SEP-2000
DEFINITION SC02_06b02_A SC02_AAFC_EC0RC_cold_stressed_winter_rye_seedlings
Scaale cereale cDNA clone SC02_06b02, mRNA sequence.
ACCESSION BE705117
VERSION BE705117.1 GI:10093382
KEYWORDS EST.
SOURCE rye.
ORGANISM Scaale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Secale.
REFERENCE 1 (bases 1 to 681)
AUTHORS Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori
,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
1. .681
/organism="Secale cereale"
/cultivar="Puma (winter rye)"
/db_xref="taxon:4550"
/clone="SC02_06b02"
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ings"
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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site.1: Eco RI;
Site.2: Xho I; Sampled three-leaf seedlings treated for
one week at 20C, 12 hrs light/day. Library made with
Stratagene UNIZAP XR Kit/(not packaged). cDNA is directly
ligated into SK+/XhoI-EcoRI, then electroporated into
TOP10 cells (Invitrogen)."
BASE COUNT 100 a 213 c 238 g 117 t
ORIGIN

Query Match 59.2%; Score 568; DB 10; Length 681;
Best Local Similarity 91.1%; Pred. NO. 9.6e-97;
Matches 621; Conservative 13; Mismatches 45; Indels 3; Gaps 3;

Qy 279 ccgcacagcgcggcgctgcctggcccaagggtttctacaactacgcgccttcgtcgccgc 338
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Qy 339 ccgcactgtctcggttcgcgaccacacaggtagcaccgcgctcaagaagcgaggt 398
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Db 623 CGCCAACTCGTCTC-GGTTTCGACACACAGGGTGCACCCGACGATCAGAGACGGCAGGT 565
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Qy 399 ggccggttctcgtcagacttccacagagacgcgcgggttgccgacgcgcgcga 458
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Qy 459 cggccctactctcctgggctactgttcaaccaggagcgcgccacactccgactactg 518
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Db 504 CGGCCCTACTCTGTTGGGCTACTGTTCAACAGGAGCGCGGCCCTCCGACTACTG 445
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Qy 519 cacgcgagctcgcagtgcccatgtgcgccggggaagaagtacttccggcgcgcccat 578
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Db 444 CTCGCGAGCTCGCAGTGGCGTGGCGCGCGGCAAGAAGTACTTTCGGGCGCGGCGCCAT 385
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Qy 579 ccagatctcacacaactacaactacggccggcgaggccatcgacacgactact 638
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Db 384 CCAGATCTCATACAACTACGAGGCGCGGGGGGCGGCAATCGCGACGACCTACT 325
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Qy 639 caacaaccggacacttggcgacgcgcgcacccgtcgtttaagcggggttggtt 698
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Qy 699 ctggtgacgcgcgaatcacccaagccttcagaccacagctgatacggcgccgtggag 758
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Db 264 CTGGATGACGCGCAGTCAACCAACCTTCGAGCCACACGCTGATCAGCGCGCGTGAG 205
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Qy 759 cccctcggcgccgaccacggcgcggggaggtgcctgggtacggtgtgatcaccaaat 818
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Db 204 CCYTCGGGGCGCGWCGAGGCKGCGGGGAGGTGCTGGGTACGCGCTATCACCAACAT 145
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Qy 819 catcaacggtgggtcagtgcgcgcgcgaggacgcgcggtgcgcgaccggtatcgg 878
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Db 144 CATCMACGCTGGGCTCGAGTGGCGCGCGGCGGAGGACGCCCTGTCGCGCACCGATGG 85
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Qy 879 gttctacaagcgtactcgacacctcttggtcagctacgtgatacgaacctgagctgta 938
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Db 84 ATCTACAAAGCGCTACTCGGCMCTCTCTCGCSTCAACTACGCBACCTGGACTGCTA 25
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Db 24 CCACCGCGCGCGTTCGCGMTAG 3
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RESULT 4
LOCUS BG365536 805 bp mRNA EST 08-MAR-2001
DEFINITION HVSMEI0003B22f Hordeum vulgare 20 DAP spike EST library HVCNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSMEI0003B22f, mRNA sequence.
ACCESSION BG365536
VERSION BG365536.1 GI:13254635
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 805)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7286
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: AATTAACTCCTACTAAAGGG
High quality sequence stop: 778.
Location/Qualifiers
1. .805
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"

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FEATURES
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HVCNA0010 (20 DAP)"
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/lab_host="SOLR"
/note="Vector: lambda2AP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT 135 a 274 c 271 g 125 t

ORIGIN

Query Match 53.7%; Score 515.8; DB 11; Length 805;
Best Local Similarity 81.8%; Pred. No. 5.5e-87;
Matches 595; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 224 gggggggtctctccattatctctgagtcgtctctctgacacagatgtgtgcacgcga 283

DB 34 GCGGAGCGGTCTCTCCATCATCTCGCGGACAGTTCGACCGCATGTTGCTGCACGCA 93

QY 284 aqagcgcggtgctggcgaagggttctacaactacgcgccttcgctgcgcgcgcga 343

DB 94 ACGACGGCCCTGCGAGGCGAGGGGTTCTACACCTACGAGCCTTCGCGCGCGCAT 153

QY 344 actggtctcgggttcgagacacaggttagcaccacgtcaagaagcgcgaggtggccg 403

DB 154 CTGCTTCGCGGCTTCGCGAGCAGCGGAGCGCGACGCCAGAGCGGAGTGGCGG 213

QY 404 cgttctcgtcaactctccacagacagacgcggcggttgccgcagcgcgcgcgcgc 463

DB 214 CPTCTCGCCAGAGCTCCACGAGACACCGCGCGGATGGGCGAGCGGACCGGCGGG 273

QY 464 cctactcctgggtactgcttcaaccagagcgcgcgcgcgcgcgcgcgcgcgcgcgc 523

DB 274 CTTCTGCGGCTACTGCTTCAAGCAGGAACGGCGCGCTCTCTCGACTACTGCACC 333

QY 524 cgaactcgcagtgccatgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 583

DB 334 CGAGCGCACAGTGGCGGTGCGCGCCCGGGAAGCGGCTACTACGCGCGCGGCGCCATCCAGC 393

QY 584 tctcacacactacaactcgc 643

DB 394 TCTCCACACTACACTATGACCTGCGCGCGCGGCGCATCGGGTCTCTCTGCGCA 453

QY 644 acccgacacttggtgc 703

DB 454 ACCCGACCTGTTGGCCACGCGCGCACCTGTGGCGTTTAAAGCGGCCATCTGTTCTGGA 513

QY 704 tgaacgcgaatcacccaagccttcgagccacgcgcgcgcgcgcgcgcgcgcgcgcgcgc 763

DB 514 TGACGGCGAGCGCGCCCAAGCCGTCGAGCCATGCTGTGATCGCGCGCGCAGTGGAGCCGT 573

QY 764 cggc 823

DB 574 CAGGGCTGACCGCGCGCAGGCGGGTGGCGGTTGGTGTGATCACCAACATCATCA 633

QY 824 acggtgggctcagtggtgc 883

DB 634 ATGTTGGGATPCGAGTGTGTCAGGACAGGACACCGCGTGTGCGCGATPCGAATCGGGTTGT 693

QY 884 acaagcctactgcgacactccttggtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 943

DB 694 ACAAGCGCTGCTGAGACATGCTGGCGCTTGCTACGGAGAGAACCTGACTGCTGTCGAGCC 753

QY 944 aaagggc 950

DB 754 AAGACCC 760

RESULT 5

RG365857

LOCUS

935 bp mRNA EST 08-MAR-2001

DEFINITION HVSME10004T09f Hordeum vulgare 20 DAP spike EST library HVCNA0010
(20 DAP), Hordeum vulgare cDNA clone HVSME10004T09f, mRNA sequence.
ACCESSION BG365857
VERSION BG365857.1 GI:13254956
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 935)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.

Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCTACTRAAGGG
High quality sequence stop: 626.

Location/Qualifiers
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/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME10004T09f"
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HVCNA0010 (20 DAP)"
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/lab_host="SOLR"

/note="Vector: lambda2AP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT 151 a 338 c 290 g 156 t
ORIGIN

Query Match 50.6%; Score 486; DB 11; Length 935;
Best Local Similarity 76.5%; Pred. No. 2e-81;
Matches 687; Conservative 0; Mismatches 200; Indels 11; Gaps 7;

QY 1 atgagaggagttgtgttggtggccatgctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 60
DB 37 ATGAGAGCGTTCGTGTGTTCGCGCGTGTTCGATGGCGGCCAGCATG---GCCGTCGCC 93

QY 61 gagcaatcggtctgcagc 120
DB 94 GAGCAGTCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 153

QY 121 ttcggtttctgcgggaaccacactccgactactgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
DB 154 TTGGGCTGTCGGGCTCCACTCGGACTACTGGCGGCGACGCGATGCCAGAGCCAGTGTCTC 213

QY 181 ggtgcagc 237
DB 214 GGCTGGCG 273

QY 238 tccattatctcgcagtcgctcttcgaccagatgctgctgcgcgcgcgcgcgcgcgcgcgcgc 297
DB 274 TCCATCGCTTCACGGCGCCCTTCGACCGCATGCTTCTCCACCGCACGACGCGCGCTGC 333

QY 298 ctggccaaagggtttctacaaactacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 357
DB 334 CAGGCCAAGGGCTTCTACACTACGAGCGCTTGTCTCGCGCGCGCGCATCCGCTTTCGCGGGC 393


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RESULT 7
BE602672 729 bp mRNA EST 02-MAR-2001
LOCUS HVSMEH0101A21f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0101A21f,
mRNA sequence.
ACCESSION BE602672
VERSION BE602672.1 GI:9860233
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 729)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence stop: 713.
Location/Qualifiers
1..729
/organism="Hordeum vulgare"
/cultivar="Morex"
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/clone="HVSMEH0101A21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 120 a 259 c 239 g 110 t 1 others
ORIGIN

Query Match 47.7%; Score 458.2; DB 10; Length 729;
Best Local Similarity 80.9%; Pred. No. 3.1e-76;
Matches 546; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 224 ggggggggtctctccattatctgcagtcgtcttcttgcacagatgctgctgcaacgca 283
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Db 56 GCGGAGCGGTGTCCTCCATCATCTCGCGGCACAGTTCGACCGCATGTGCTGCACCGCA 115
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QY 284 acgacggcggtgcttgcgaagggtttctacaactagcgcccttcgacgcgcgca 343
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Db 116 ACAGCGGCGCTGCCAGGCGACAGGCTTCTACACCTTACACCGCTTCGTGCGCGCGCAT 175
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QY 344 actcgttctcgggttcggacacaggttagcaccgacgtcgaagacggcgaggtgccc 403
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Db 176 CTGCGCTTCCGGGCTCGCAGCAGCGGAGCGCCGACGCCAGAGCGCGAGGTGGCGG 235
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QY 404 cgttctcgtcagacttccacagacacggcggtgtggccgacggcgcccgacggcc 463
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Db 236 CCTTCTTGCCCGACAGCTCCACGAGACACCGCGGATGGGCGACGGCAGCGACGGG 295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 464 cctaactctggggtactgcttcaaacaggagggcgcccaactccgactactgcaagc 523
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296 CCTTCGCTGGGCTACTGCTTCAAGCAGGAACGCGGCGCTCTCTCGACTACTGCACCC 355
QY 524 cgactcgcaatgccaatgtgcgcgggcaagaagtacttcggcgcgggcccatcagca 583
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Db 356 CGAGCGCACAGTGGCGGTGCGCCCCCGGGAAGCCTACTAGCGCGGGGGCCCATCCAGC 415
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QY 534 tctcacacaactacaactacggcgcgcgggcaggccatcgccacggacgtgtcaca 643
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Db 416 TCTCCACACACTACAACCTATGACCTGCGGCGCGGCATCGGGGTGATCTGCTGGCCA 475
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QY 644 accggacacctgtggctggcgacgcgacgtgtcgtttaagaacggcgttgtgtctaga 703
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Db 476 ACCGGGAGCTGTGGTGGCCACGACGCCACTGTGGCGGTTTAAAGACGCCCATCTGGTTCTGGA 535
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QY 704 tgacgcgcgaatcaccccaagccttcgagccacgacgtgatcacggcgcggtggagccct 763
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QY 764 cggcgccgcacacgagcgcgcggggaggggtgcctgtggtgacggtgtgataccaacatca 823
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QY 824 acgttggtcgagtcggcgcgggcgagcgcggtgtcgccgacggatcggttct 883
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Db 656 ATGCTGGGATCGATGTGTCACGGACAGGACAGCCCGCTGCCGATCGAATC-GGTTTT 714
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QY 884 caagcgctactgog 898
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Db 715 ACAAGCGTACTGTG 729
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RESULT 8
BG365887 937 bp mRNA EST 08-MAR-2001
LOCUS HVSMEI0004K07f Hordeum vulgare 20 DAP spike EST library HVCNDA0010
DEFINITION (20 DAP) Hordeum vulgare cDNA clone HVSMEI0004K07f, mRNA sequence.
ACCESSION BG365887
VERSION BG365887.1 GI:13254986
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 937)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence stop: 888.
Location/Qualifiers
1..937
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEI0004K07f"
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/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
FEATURES
source

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/clone_lib="Hordeum vulgare 20 DAP spike EST library
HvCDNA0010 (20 DAP)"
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/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ to
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 106 a 223 c 202 g 93 t 1 others
ORIGIN

Query Match 43.8%; Score 420.6; DB 11; Length 625;
Best Local Similarity 80.6%; Pred. No. 3.2e-69;
Matches 503; Conservative 0; Mismatches 120; Indels 1; Gaps 1;
QY 235 tctccattatctcgcagtcgctcttcgaccagatgctgtcacgcacgacgagcgcg 294
DB 2 TCTCCATCGTCTCAGCGGCCCTTTTCGACCGCATGCTTTTCACCGCCACCAACGGCGC 61
QY 295 tgcctggcaagggtttctacaactacggcgcttctgtgcgcgcgcgcacactggttcg 354
DB 62 TGGCAGGCCAAGGCTCTACACCTACGACGCTTGTGCGCCCGGAAATCCGCTTCGG 121
QY 355 ggcttcgacacagtagcaccgagctcaagaagcgagtggtgacgagtcctcgt 414
DB 122 GGTTCGGCACCAACCGCGGAGACGACACCGGAGCGAGGTGCGGCTTCTCCGGCC 181
QY 415 cagacttccacagacgacgagcggtggtgacgagcgcgccgacgcccactactctg 474
DB 182 CAAACCTCCACAGACACCGCGGCTGGCGACGCGACCGACGAGGTTTCGCTGG 241
QY 475 ggctactgttcaacagagcggtggtgacacactcgcactactgacgagcgagtcgag 534
DB 242 GGCTACTGTTCAAGCAGGAGCGTGGCGCCACCTCCAACTACTGCACTCCGAGCGCGAG 301
QY 535 tggcctggtcgccgggcaagaagtacttgcggcggtggtggtggtggtggtggtggtggt 594
DB 302 TGGCCGTGGCCGCCAGGAGAGCTACTAGCGCGGTGGCGGCGATCCAGCTCTCCCAAC 361
QY 595 tacaactagcgccggcggtggtggtggtggtggtggtggtggtggtggtggtggtggt 654
DB 362 TACAACCTAGCGGCTTGGGCGCGGCGCATCGGGGTGACCTTCTGCGACACCGGACCTG 421
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DB 422 GTGGCCACGACCGACCGGTGCTGTATAGACTGCGATGTGTGTGTGTGTGTGTGTGTGT 481
QY 715 tcaaccaagcttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 774
DB 482 GCGCCAAAGCGTGCAGCCATGCTGTATCAGCGGCGAGTGGAGCCCATCAGGACGGAC 541
QY 775 caggcgcggtgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 833
DB 542 CGGCGACGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTG 601
QY 834 cgagtcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 857
DB 602 CGAGTGGCGCATGGGAGGACAG 625

RESULT 15
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LOCUS HVSMH0093N17f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HvCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMH0093N17f,
mRNA sequence.
ACCESSION BE454366
VERSION BE454366.2 GI:13189266
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 969)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
On Jul 26, 2000 this sequence version replaced gi:9462873.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCTACTAAAGG
High quality sequence stop: 616.
Location/Qualifiers
1..969
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMH0093N17f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HvCDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ to
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT 194 a 312 c 280 g 181 t 2 others
ORIGIN

Query Match 43.4%; Score 416.2; DB 10; Length 969;
Best Local Similarity 77.0%; Pred. No. 2.2e-68;
Matches 535; Conservative 0; Mismatches 150; Indels 10; Gaps 2;
QY 224 gggcggtctctccattatctcagtcgctcttcgaccagatgctgtcacgca 283
DB 128 GCGGACGCTGCTTCCATCATCTCGCGCGCACAGTTTCGACCGCATTTGCTGACCGCA 187
QY 284 acgacggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 343
DB 188 AGCAGCGGCTGCCAGGCCAAGGGCTTCTACACTACGACGCTTCTGCGCGCGCAT 247
QY 344 actgttctcggttcgacacacaggttagcaccagcagcagcagcagcagcagcagcagc 403
DB 248 CTGCTTCCGGGCTTCGCGACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
QY 404 cgttctctgtagacttccacagacgacgagcagcagcagcagcagcagcagcagcagc 463
DB 308 CCTTCTTGGCCCGACCTCCACGAGACCCGCGGATGGCGGACCGGACCGCGCGGG 367
QY 464 ctactctgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 514
DB 368 CTTTCGCTGGGGCTACTGGGCTTTTCCCAAAACAGGAAACGCGCGCGCTCTCCGACT 427
QY 515 actgcacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 574
DB 428 ACTGCACCGGAGCGCACAGTGGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
QY 575 ccatcagatctcaacaactacacgagcagcagcagcagcagcagcagcagcagcagcagc 634
DB 488 CCATCCAGCTCTCCCAACTAGAACTATGACCTGCTGCGCGCGCGCGCGCGCGCGCG 547
QY 635 tgcctcaaacacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 694
DB 548 TGTGGCCACCGGACCTGTTGGCCACGAGCGGCGCGCGCGCGCGCGCGCGCGCGCG 607

695	ggtctgtagacgcgcgcaatcacccaagcctctagaccagcaogtgcac-acgggcgcgg	753
QY		
698	GGTTCGGATGACGGCGCANCGCCCAAGCCGTCGAGCATGCTGTGATCGCCGCCCCAG	667
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754	tggagcccttcgggcgcgcacacagcgcgggagggtgcctggtaacgggtgtgatacc	813
QY		
668	TGAGGCCGTTAAGGCTGACCGGCCGCAAGCGGGTCCCGGTTTGGTGTATCAC	727
Db		
814	ascatcatcaacggtgggtcgagtgcggcgcggcagcagcgccgtgtgcgcacagg	873
QY		
728	CACATCATTAATGGGGGATTCAATGTGTACCGACCGAGAAACCGTTTCGNCAICCA	787
Db		
874	atcgggttctacaagcgtactgcgacctcttgg	908
QY		
788	AATGGTTTTACAAGCGCTCTGGGACTTCCTCGG	822
Db		

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